



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 95712

TO: Shin-Lin Chen
Location: cm1/12a15/12e12
Art Unit: 1632

June 6 2003

Case Serial Number: 788188

From: P. Sheppard
Location: CM1-1E03
Phone: (703) 308-4499

sheppard@uspto.gov

Search Notes

Qy 181 DENPVDSGCGIDSKHNSYCTTHTFVKALTMDSKQAAFRIRIDTACVLSKAAVR 240
 |||
 Db 226 DENPVDSGCGIDSKHNSYCTTHTFVKALTMDSKQAAFRIRIDTACVLSKAAVR 285
 |||
 Qy 241 A 241
 |||
 Db 286 A 286

RESULT 2

14614
 nerve growth factor B - pig (fragment)
 C/Species: Sus scrofa domestica (domestic pig)
 C/Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 16-Jul-1999
 C/Accession: 146614
 R/Label: Marnett, Y., Mellink, C., Yezle, M., Gellin, J.
 C/Genetic: Cell Genet. 67, 120-125, 1994
 A/Title: A new marker (NGFB) on pig chromosome 4, isolated by using consensus sequence
 A/Reference number: 146614; MUID:94313891; PMID:8039422
 A/Accession: 146614
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-229 <LAH>
 A/Cross-references: GB:L31898; NID:9476732; PIDN:AAA21301.1; PID:9533771
 C/Genetics:
 A/Gene: NGFB
 C/Superfamily: nerve growth factor beta chain

Query Match 88.2%; Score 1119; DB 2; Length 229;
 Best Local Similarity 92.1%; Pred. No. 1.3e-97;
 Matches 211, Conservative 5, Mismatches 13, Indels 0, Gaps 0;
 Qy 13 LIGQAEHSHSNVPAAGHTTPOVWTKLQHSIDTLARRAPAAIAAAYAGTNTIV 72
 |||
 Db 1 LIGQAEHSHSNVPAAGHTTPOVWTKLQHSIDTLARRAPAAIAAAYAGTNTIV 60
 |||
 Qy 73 DPLFKKRLASPRVLFSTOPPREADTODLDFVGAAPSRTHSGSSHPFRGE 132
 |||
 Db 61 DPLFKKRLASPRVLFSTOPPREADTODLDFVGAAPSRTHSGSSHPFRGE 120
 |||
 Qy 133 FSVCDVSVMVGDKTATADIKGEKVMVLGEVNNINSVFQYFFETKCRDPNPVDSGCGI 192
 |||
 Db 121 FSVCDVSVMVGDKTATADIKGEKVMVLGEVNNINSVFQYFFETKCRDPNPVDSGCGI 180
 |||
 Qy 193 DSKHNSYCTTHTFVKALTMDSKQAAFRIRIDTACVLSKAAVR 241
 |||
 Db 181 DSKHNSYCTTHTFVKALTMDSKQAAFRIRIDTACVLSKAAVR 229
 |||

RESULT 3

156570
 beta-nerve growth factor - rat (fragment)
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 16-Jul-1999
 C/Accession: 156570
 R/Label: Marnett, S.R., Friedman, P.L., Larhammar, D.G., Persson, H., Gonzalez-Carvajal, M.,
 J. Neurosci. Res. 20, 403-410, 1988
 A/Title: Rat beta-nerve growth factor sequence and site of synthesis in the adult hippo
 A/Reference number: 156570; MUID:89037223; PMID:3184206
 A/Accession: 156570
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-245 <RBS>
 A/Cross-references: GB:M36589; NID:9205691; PIDN:AAA41697.1; PID:9205692
 C/Superfamily: nerve growth factor beta chain

Query Match 86.9%; Score 1102; DB 2; Length 245;
 Best Local Similarity 85.4%; Pred. No. 5.8e-96;
 Matches 205, Conservative 15, Mismatches 20, Indels 0, Gaps 0;
 Qy 1 MSMLFYLITLFAIGQAEHSHSNVPAAGHTTPOVWTKLQHSIDTLARRAPAAIAA 60
 |||
 Db 1 MSMLFYLITLFAIGQAEHSHSNVPAAGHTTPOVWTKLQHSIDTLARRAPAAIAA 60
 |||

Db 5 MSMLFYLITLFAIGQAEHSHSNVPAAGHTTPOVWTKLQHSIDTLARRAPAAIAA 64
 |||
 Qy 61 ARVAGQTRNTIVDRRLFKKRLASPRVLFSTOPPREADTODLDFVGAAPSRTHSG 120
 |||
 Db 65 ARVAGQTRNTIVDRRLFKKRLASPRVLFSTOPPREADTODLDFVGAAPSRTHSG 124
 |||
 Qy 121 RSSHPIFHHGEFVCDVSVMVGDKTATADIKGEKVMVLGEVNNINSVFQYFFETKCR 180
 |||
 Db 125 RSSHPIFHHGEFVCDVSVMVGDKTATADIKGEKVMVLGEVNNINSVFQYFFETKCR 184
 |||
 Qy 181 DENPVDSGCGIDSKHNSYCTTHTFVKALTMDSKQAAFRIRIDTACVLSKAAVR 240
 |||
 Db 185 APNVESGCGIDSKHNSYCTTHTFVKALTMDSKQAAFRIRIDTACVLSKAAVR 244
 |||

RESULT 4

NGMSG
 nerve growth factor beta chain precursor - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 30-Nov-1980 #sequence_revision 19-Feb-1984 #text_change 21-Jul-2000
 C/Accession: A93301; A93305; A90366; 149689; 152891; A01400; 149690
 R/Scott, J., Selby, M., Urdia, M., Quiroga, M., Bell, G.I., Rutter, W.J.
 Nature 302, 538-540, 1983
 A/Title: Isolation and nucleotide sequence of a cDNA encoding the precursor of mouse
 A/Reference number: A93301; MUID:83167518; PMID:6336309
 A/Accession: A93301

A/Molecule type: mRNA
 A/Residues: 1-307 <SCO>
 A/Cross-references: GB:V00836; NID:953364; PIDN:CAA24221.1; PID:953365
 R/Ullrich, A., Gray, A., Berman, C., Dull, T.J.
 Nature 303, 821-825, 1983
 A/Title: Human beta-nerve growth factor gene sequence highly homologous to that of mo
 A/Reference number: A93305; MUID:83244969; PMID:6688123
 A/Accession: A93305
 A/Molecule type: mRNA
 A/Residues: 1-307 <UHL>
 A/Cross-references: GB:K01759; NID:9200051; PIDN:AAA3820.1; PID:9387495
 A/Note: these authors believe that Met-6 is probably the amino-terminal residue and
 R/Angelini, R.H., Hermanson, M.A., Bradshaw, R.A.
 Biochemistry 12, 100-115, 1973
 A/Title: Amino acid sequences of mouse 2.5S nerve growth factor. II. Isolation and ch
 A/Reference number: A90366; MUID:73075048; PMID:4566923
 A/Accession: A90366
 A/Molecule type: protein
 A/Residues: 188-216, 'N', 218-305 <ANG>
 R/Selby, M.J., Edwards, R., Sharp, F., Rutter, W.J.
 Mol. Cell. Biol. 7, 3057-3064, 1987
 A/Title: Mouse nerve growth factor gene: Structure and expression.
 A/Reference number: 149689; MUID:88038855; PMID:3670305
 A/Accession: 149689
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-307 <RBS>
 A/Cross-references: GB:M17298; NID:9193493; PIDN:AAA7687.1; PID:9467311
 R/Ullrich, A., Gray, A., Berman, C.H., Consensus, U., Dull, T.J.
 Cold Spring Harb. Symp. Quant. Biol. 48, 435-442, 1983
 A/Title: Sequence homology of human and mouse beta-NGF subunit genes.
 A/Reference number: 152891; MUID:84206565; PMID:6327169
 A/Accession: 152891
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-307 <RBS>
 A/Cross-references: GB:M14805; NID:9200053; PIDN:AAA9821.1; PID:9200054
 C/Comment: The active molecule is a dimer of identical chains associated by noncovalen
 C/Keywords: Nerve growth factor is found in submaxillary gland in large quantities and
 nic sensory ganglia in vivo and in vitro and to increase cellular neurotubule levels
 C/Genetics:
 A/Gene: NGFB
 A/Intons: 21/2, 62/3
 C/Superfamily: nerve growth factor beta chain
 F/Keywords: glycoprotein; growth factor; homodimer
 F/1-187/Domain: signal sequence and propeptide #status predicted <SIG>
 F/188-305/Product: nerve growth factor beta chain #status experimental <MAT>

A/Accession: S12532
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 126-243 <IBA>
C/Superfamily: nerve growth factor beta chain
C/Keywords: growth factor
F/1-125/Domain: signal sequence #status predicted <Sig>
F/126-243/Product: nerve growth factor beta chain #status predicted <MAT>

Query Match	61.8%;	Score 783.5;	DB 2;	Length 243;
Best Local Similarity	64.5%;	Pred. No. 4.9e-66;		
Matches 160;	Conservative 21;	Mismatches 48;	Indels 19;	Gaps 6;

QY 1 MSMLFTLLTAFLIGIOAEPHESN-----VPAGHTIPQVHTKQHSUDTLAPARASAPA 56
QY 5 MSMLYTTLLIAFLIGIOAPKSEDNQPLEYPLMHSBLPQSQNGH-----AKAAPQ 57
QY 57 AALAAVA-----GQTRNI TVDPRLFKKRLRLSPVLVSTOPPPEAADTODLDFEVGAA 111
Db 58 TT-HGFAPAMPDQTBELTNAMQONFPKKRFFSSVFLSTQBPVPVSRKQSGTG-LSAV 115
QY 112 PFERTSRKSSSHPIFRHGEPSCVDSVWVGDKTATDILKGEVWMLGAVNNINSVFK 171
Db 116 SLNRITARTGR-TAHPVLRHGEPSCVDSVSWVGDKTATDILKGEVTVLGLGVNNINNVFK 174
QY 172 QYFETKCDPNPVDGCGRIDSKMNSYCTTHTFVALTMDGKOAMREIRIDTACVC 231
Db 175 QYFETKCDPRPVSSGCGRIDAKMNSYCTTHTFVALTMEGQOAMRIRIDTACVC 234
QY 232 VLSRKAVR 239
Db 235 VLSRSGR 242

RESULT 8
S14481

C/Species: Xenopus laevis (African clawed frog)
 C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 16-Jul-1999
 C/Accession: S14481
 R/Cartero, F.; Camion, M.; Cardinali, B.; Pierandrei-Amaldi, P.
 submitted to the EMBL Data Library, October 1990
 A/Description: Structure and expression of the nerve growth gene in Xenopus oocyte and e
 A/Reference number: S14481
 A/Accession: S14481
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-235 <CNR>
 A/Cross-references: EMBL:X55716, NID:g64914, PIDN:CAA39249.1, PID:g64915
 C/Superfamily: nerve growth factor beta chain

Query Match	60.6%	Score 768	DB 2	Length 235
Best Local Similarity	63.2%	Pred. No. 1.3e-64		
Matches 153; Conservative	28	Mismatches 41	Indels 20	Gaps 6

[illegible]

D_b 231 RK 232

RESULT 9
TEST 1991

nerve growth factor precursor - many-banded krait
 C/Species: Bungarus multicinctus (many-banded krait)
 C/Date: 13-Sep-1996 #sequence_rev151193
 C/Accession: 151193
 R/Danse, J.M.; Garnier, J.M.
 Growth Factors 8, 77-86, 1993
 A/Title: Molecular cloning of a cDNA encoding a nerve growth factor precursor from the
 A/Reference number: 151193; MOID:93192074; PMID:7916740
 A/Accession: 151193
 A/Status: preliminary; translated from GB/EMBL/DBD
 A/Molecule type: mRNA
 A/Residues: 1-243 <DAN>
 A/Cross-references: GB:SS6212; NID:g266298; PIDN:AAB5729.1; PID:g266299
 C/Superfamily: nerve growth factor beta chain

Query Match	53.0%;	Score 671.5;	DB 2;	Length 243;
Best Local Similarity	-56.1%;	Pred. No. 1.6e-55;		
Matches 138; Conservative	29;	Mismatches 62;	Indels 17;	Gaps 5

Qy	1	MSMTEYTTITLTFVLGICQEPSESNVAG-----HTIPQVMTKLOHSLDPALEARRASAPA	56
Db	1	MSMLCYTIIILFLGIVMAAPKSEEDNVLGSPASDSEFDNTCAQCHBELKTSRNTDQHPT	60
Qy	57	AAIAA-RVAGQTRNTITVDPFLFKKRLRLSPVLFTSTOPPREADTD--LDPEVGGAAP	112
Db	61	PKKSDSDGLGAANIIYDPPKLFQRRRPQSPVLFSTPPPLSRDEGVKFLDTE-----	114
Qy	113	FSRTRRS--KRSSSHPIFHGEFECVCSVSWVGDKTATDINGKEVMVLGEVINNSVF	170
Db	115	-DILAKRIKMANNEHVPVHNOGSEHSCDISISWVINKKATDIGNVTVVAVDNLINNEY	173
Qy	171	KQYFEETKCRDPNVNDSGCRGIDSKHNSYCTTTHFVKALTMNDGKOAAARFTRIDTACV	230
Db	174	KQYFEETKCRPNPEVPGCGRGIDSRHNSYCTTTDFVVKALTMNGRAISRFRTRIDTACV	233
Qy	231	CVLSRK	236
Db	234	CVLSRK	239

RESULT 10

Nerve growth factor beta chain precursor - bovine (fragment)
 C.Species: Bos primigenius taurus (cattle)
 C.Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 16-Jul-1999
 C.Accession: A26312
 R.Meiler, R.; Becker-Andre, M.; Goetz, R.; Heumann, R.; Shaw, A.; Thoenen, H.
 EMBO J. 5, 1489-1493, 1986
 A.Title: Molecular cloning of bovine and chick nerve growth factor (NGF): delineation
 A.Reference number: A26312; MUID:86300647; PMID:2427334
 A.Accession: A26312
 A.Molecule type: mRNA
 A.Residues: 1-125 <ME>
 A.Cross-references: GB:M26809; NID:G163419; PIDN:AAA30666.1; PID:G163420
 C.Comment: Nerve growth factor stimulates neurite outgrowth from sympathetic and embry-
 C.Superfamily: nerve growth factor beta chain
 C.Keywords: growth factor; homodimer; genital vesicle
 F.6-125/Product: nerve growth factor #status predicted <MAT>
 F.20-85,63-113,73-115/Diulfide bonds: #status predicted

Query Match	51.9%	Score 658;	DB 2;	Length 125;
Best Local Similarity	95.2%;	Pred. No. 1.3e-54;		
Matches 119; Conservative	4;	Mismatches 2;	Indels 0;	Gaps 0

117 HRSKRSSSHIFHRGEFVSVDSSVMTGDKTTATDIKGEVMTLGEVNNINSVFKQYFFE 176
1 HRSKRSSSHVFEHRGEFVSVDSSVMTGDKTTATDIKGEVMTLGEVNNINSVFKQYFFE 60

QY 177 TKCDPVPVDSGCGIDSKMNSYCTTTHFVKALTMGQKQAAFRIRIDPACVLSRK 236
DB 61 TKCDPVPVDSGCGIDSKMNSYCTTTHFVKALTMGQKQAAFRIRIDPACVLSRK 120
QY 237 AVBRA 241
DB 121 TQORA 125

RESULT 11

A59218

nerve growth factor beta chain precursor - monocled cobra

C/Species: Naja naja kaouthia, Naja naja siamensis (monocled cobra)

C/Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 31-Mar-2000

C/Accession: A59218, S13965

R/Selby, M.J.; Edwards, R.H.; Rutter, W.J.

J. Neurosci. Res. 18, 293-298, 1987

A/Title: Cobra nerve growth factor: structure and evolutionary comparison.

A/Reference number: A59218; PMID:88090976; PMID:3694712

A/Accession: A59218

A/Molecule type: mRNA

A/Residues: 1-246 <SEL>

R/Inoue, S.; Oda, T.; Koyama, J.; Ikeda, K.; Hayashi, K.

FEBS Lett. 279, 38-40, 1991

A/Title: Amino acid sequences of nerve growth factors derived from cobra venoms.

A/Reference number: S13927; PMID:91138755; PMID:1995338

A/Accession: S13965

A/Molecule type: protein

A/Residues: 131-246 <INQ>

A/Experimental source: Venom

C/Comment: Nerve growth factor is necessary for the development of embryonic sympathetic

C/Complex: homodimer

C/Superfamily: nerve growth factor beta chain

F.1-23/Domain: signal sequence #status predicted <SIG>

F.131-246/Product: nerve growth factor beta chain #status experimental <MAT>

F.144-208, 186-236, 196-238/Distulfide bonds: #status predicted

Query Match

Best Local Similarity 50.8%; Score 644; DB 2; Length 246;

Matches 133; Conservative 31; Mismatches 69; Indels 8; Gaps 5;

QY 1 MSMFLYTLITATLIGIOAPHSSESNVPAQ---HTIPQVHWTKQHSIDTALBRASAPA 56
DB 6 MSMFLYTLITATLIGIOAPHSSESNVPAQ---HTIPQVHWTKQHSIDTALBRASAPA 65
QY 57 AAIARVAGQT-RNTTVDPRFLFKKRLRSFVLPSTOPPREADTQDLDFEYGAAPFAR 115
DB 66 FOKEDQELRTFANIIYDPLFKFOKQPOSPFLVFTQPLSLRDESVF-LDNEDSLNR 124
QY 116 THRSRSSHPIPHRGESVCDVSVMWGDKTATADIKKEVWVAGEVINNSVFQYF 175
DB 125 NTRAKR-BDHVPHNIGHSVCDVSVMWGDKTATADIKKEVWVAGEVINNSVFQYF 182
QY 176 ETTCRDPVPVDSGCGIDSKMNSYCTTTHFVKALTMGQKQAAFRIRIDPACVLSRK 235
DB 183 ETTCRDPVPVDSGCGIDSKMNSYCTTTHFVKALTMGQKQAAFRIRIDPACVLSRK 242
QY 236 K 236
DB 243 K 243

RESULT 12

S28161

nerve growth factor beta chain - Russell's viper

C/Species: Vipera russelli (Russell's viper)

C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Oct-1997

C/Accession: S28161

R/Koyama, J.; Inoue, S.; Ikeda, K.; Hayashi, K.

Biochim. Biophys. Acta 1160, 287-292, 1992

A/Title: Purification and amino-acid sequence of a nerve growth factor from the venom of

A/Reference number: S28161; PMID:93120151; PMID:1477101

A/Accession: S28161
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-117 <KOY>
C/Superfamily: nerve growth factor beta chain

Query Match 38.2%; Score 484; DB 2; Length 117;
Best Local Similarity 74.1%; Pred. No. 2.8e-38;
Matches 83; Conservative 19; Mismatches 10; Indels 0; Gaps 0;

QY 125 HPFHRGEFVCDVSVMWGDKTATADIKKEVWVAGEVINNSVFQYFETKCRDPNP 184
DB 1 HPFHRGEFVCDVSVMWGDKTATADIKKEVWVAGEVINNSVFQYFETKCRDPNP 60
QY 185 VDSGCGIDSKMNSYCTTTHFVKALTMGQKQAAFRIRIDPACVLSRK 236
DB 61 VDSGCGIDSKMNSYCTTTHFVKALTMGQKQAAFRIRIDPACVLSRK 112

RESULT 13

I51709

nerve growth factor beta chain precursor - southern platyfish

C/Species: Xiphophorus maculatus (southern platyfish)

C/Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Jul-1999

C/Accession: I51709, S26674

R/Goetz, R.; Raulf, F.; Schardt, M.

J. Neurochem. 59, 432-442, 1992

A/Title: Brain-derived neurotrophic factor is more highly conserved in structure and fi

A/Reference number: I51709; PMID:92333301; PMID:1629719

A/Accession: I51709

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-194 <GOT>

A/Cross-references: EMBL:X59941; NID:G65277; PDB:CAA42566.1; PID:G65278

C/genetics:

A/Gene: NGF

C/Superfamily: nerve growth factor beta chain

C/Keywords: glycoprotein; growth factor

F.1-14/Domain: signal sequence #status predicted <SIG>

F.15-79/Domain: propeptide #status predicted <PRO>

F.80-194/Product: nerve growth factor beta chain #status predicted <MAT>

F.90-155, 133-183, 143-185/Distulfide bonds: #status predicted

F.199/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match

Best Local Similarity 38.0%; Score 481.5; DB 2; Length 194;

Matches 99; Conservative 14; Mismatches 39; Indels 15; Gaps 3;

QY 71 TVDPRFLFKKRLRSFVLPSTOPPREADTQDLDFEYGAAPFSTRSRSSHPFIR 130
DB 40 TVDPRFLFKKRLRSFVLPSTOPPREADTQDLDFEYGAAPFSTRSRSSHPFIR 84
QY 131 GEFVCDVSVMWGDKTATADIKKEVWVAGEVINNSVFQYFETKCRDPNPVDSGR 190
DB 85 GEFVCDVSVMWGDKTATADIKKEVWVAGEVINNSVFQYFETKCRDPNPVDSGR 144
QY 191 GIDSKMNSYCTTTHFVKALTMGQKQAAFRIRIDPACVLSRK 237
DB 145 GIDSKMNSYCTTTHFVKALTMGQKQAAFRIRIDPACVLSRK 191

RESULT 14

C40304

neurotrophin-3 precursor - human

N/Alternate names: nerve growth factor 2; NGF-2

C/Species: Homo sapiens (man)

C/Date: 03-Apr-1992 #sequence_revision 30-Sep-1993 #text_change 16-Jul-1999

C/Accession: A36208; J0141; C40304; S10719; C60536

R/Jones, K.R.; Reichardt, L.F.

Proc. Natl. Acad. Sci. U.S.A. 87, 8060-8064, 1990

A/Title: Molecular cloning of a human gene that is a member of the nerve growth factor

A/Reference number: A36208; PMID:91045937; PMID:2236018

A/Accession: A36208

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 6, 2003, 10:47:28 ; Search time 27 Seconds

(without alignments)
1839.161 Million cell updates/sec

Title: US-09-788-188-1
Perfect score: 1270
Sequence: 1 MSMLFYTITATLIGIQAE.....FIRIDNACVLSRAKVRRA 241

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 10%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL 21: *
1: sp_archaea: *
2: sp_bacteria: *
3: sp_fungi: *
4: sp_human: *
5: sp_invertebrate: *
6: sp_mammal: *
7: sp_mbc: *
8: sp_organelle: *
9: sp_phage: *
10: sp_plant: *
11: sp_rodent: *
12: sp_virus: *
13: sp_vertebrate: *
14: sp_unclassified: *
15: sp_virus: *
16: sp_bacterioid: *
17: sp_archaeap: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1266	99.7	241	4	Q9UKL8
2	1265	99.6	241	4	Q9P2Q8
3	1258	99.1	241	4	Q96P60
4	1249	98.3	241	6	Q9N2P0
5	1248	98.3	241	6	Q9N2P1
6	1247	98.2	241	6	Q9N2P2
7	1132	89.1	217	6	Q9N1B3
8	1038	81.7	294	11	Q91XB4
9	713	56.1	241	13	Q9DBZ9
10	709	55.8	241	13	Q9DBZ8
11	462	36.4	87	4	Q9PTC3
12	459	36.1	87	4	Q9P2Z4
13	449.5	35.4	132	11	Q9W015
14	426.5	33.6	241	6	Q9N1B2
15	426	33.5	286	13	Q91988
16	363	28.6	247	6	Q97759

17	360	28.3	249	11	Q8VHH4	Q8VHH4 mus musculus
18	342.5	27.0	246	13	Q8G374	Q8G374 cyclophorus
19	341.5	26.9	246	13	Q8G376	Q8G376 jalapura sp
20	339.5	26.7	270	13	Q9YH42	Q9YH42 brachydactyl
21	335.5	26.4	246	13	Q8G375	Q8G375 phrynosoma
22	334.5	26.3	153	11	Q9CYL2	Q9CYL2 mus musculus
23	331.5	26.1	177	13	Q91BL2	Q91BL2 poephila gu
24	319	25.1	247	13	Q8G377	Q8G377 tylosotriton
25	294.5	23.2	101	6	Q9TF22	Q9TF22 macaca fusc
26	293	23.1	324	13	Q9XY95	Q9XY95 lampetra fl
27	291	22.9	186	12	Q9J5D9	Q9J5D9 fowipox vir
28	242	19.1	52	6	Q9N1V4	Q9N1V4 equus caball
29	226	17.8	85	6	Q02790	Q02790 macropus fu
30	224	17.6	42	6	Q02802	Q02802 trichosurus
31	220	17.3	85	6	Q13114	Q13114 isodon mac
32	220	17.3	85	6	Q13122	Q13122 tarsipes ro
33	220	17.3	85	6	Q02795	Q02795 ornithorhyn
34	220	17.3	85	6	Q02798	Q02798 petaurus br
35	220	17.3	85	6	Q13104	Q13104 cercartetus
36	220	17.3	85	6	Q02792	Q02792 notoryctes
37	220	17.3	85	6	Q13105	Q13105 dasynotoides
38	220	17.3	85	6	Q02801	Q02801 tachylosau
39	219	17.2	85	6	Q02803	Q02803 trichosurus
40	211	16.6	42	6	Q02794	Q02794 ornithorhyn
41	209	16.5	42	6	Q02800	Q02800 tachylosau
42	178.5	14.1	186	6	Q9BFJ4	Q9BFJ4 lemur catra
43	178.5	14.1	186	11	Q9NMT1	Q9NMT1 castor cana
44	176.5	13.9	186	6	Q9BFJ7	Q9BFJ7 octotoma hy
45	175	13.8	185	6	Q9BFK6	Q9BFK6 talpa talai

ALIGNMENTS

RESULT 1

Q9UKL8 PRELIMINARY; PRT; 241 AA.
ID Q9UKL8;
AC 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Nerve growth factor B.
GN NGFB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9256269; PubMed=10322959;
RA Tong Y., Wang H., Chen W.;
RT "Cloning and sequencing of the gene for premature beta nerve growth factor.",
RL Chung Kuo Ying Yung Sheng Li Hsueh Tsa Chih 13:316-318 (1997).
RN [2]
RP SEQUENCE FROM N.A.
RA Tong Y., Wang H.;
RL Submitted (May-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL, AF150960; AAD55975.1; -;
DR HSSP, P01139; 1BET.
DR InterPro, IPR02072; NGF.
DR Pfam, PF00243; NGF, 1.
DR PRINTS, PR00268; NGF.
DR PRODOM, PD002052; NGF, 1.
DR SMART, SMO0140; NGF, 1.
DR PROSITE, PS00246; NGF_1; 1.
DR PROSITE, PS00270; NGF_2; 1.
SQ SEQUENCE 241 AA; 2699 MW; 619DFC5EB3BD671 CRC64;
Query Match 99.7%; Score 1266; DB 4; Length 241;
Best Local Similarity 99.6%; Pred. No. 8.3e-117;
Matches 240; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 MSMLFTTLTAFLIGIOAEPHSESNVPAAGHTIPQVWMTKQHSJLDTALRRASAPAAIA 60
DB 1 MSMLFTTLTAFLIGIOAEPHSESNVPAAGHTIPQVWMTKQHSJLDTALRRASAPAAIA 60
QY 61 ARVAGQTRNITVDPRLFKKRRLSPRVLPSTQPPREADTODLDEVEGGAAPFNTRHSK 120
DB 61 ARVAGQTRNITVDPRLFKKRRLSPRVLPSTQPPREADTODLDEVEGGAAPFNTRHSK 120
QY 121 RSSSHPIFRGSESVCDVSVMVGDKTTATDIDKGEVWVLGEVINNSVFKQYFPETKCR 180
DB 121 RSSSHPIFRGSESVCDVSVMVGDKTTATDIDKGEVWVLGEVINNSVFKQYFPETKCR 180
QY 181 DPNPVDSCGRGIDSKHMSYCTTHTFVKALTMDSKQAAWRFIRIDTACVCLSRKAVRR 240
DB 181 DPNPVDSCGRGIDSKHMSYCTTHTFVKALTMDSKQAAWRFIRIDTACVCLSRKAVRR 240
QY 241 A 241
DB 241 A 241

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RESULT 2

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Q9P208 PRELIMINARY; PRT; 241 AA.
ID Q9P208
AC Q9P208
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE Beta-nerve growth factor (Fragment).
GN Beta-NGF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCB1_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RA Kltano T., Kobayakawa H., Saitou N.;
RT "Silver Project.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB037517; BAA90437.1; -.
DR HSBP; P01139; ISET.
DR InterPro; IPR02072; NGF.
DR Pfam; PF00243; NGF.
DR PRINTS; PR00268; NGF.
DR Prodom; PD002052; NGF.
DR SMART; SM00140; NGF.
DR PROSITE; PS00248; NGF_1; 1.
DR PROSITE; PS50270; NGF_2; 1.
DR NON TER 241
SQ SEQUENCE 241 AA; 26998 MW; D531ED825D96C14 CRC64;

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Query Match 99.6%; Score 1265; DB 4; Length 241;
Best Local Similarity 99.6%; Pred. No. 1e-116;
Matches 240; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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```

QY 1 MSMLFTTLTAFLIGIOAEPHSESNVPAAGHTIPQVWMTKQHSJLDTALRRASAPAAIA 60
DB 1 MSMLFTTLTAFLIGIOAEPHSESNVPAAGHTIPQVWMTKQHSJLDTALRRASAPAAIA 60
QY 61 ARVAGQTRNITVDPRLFKKRRLSPRVLPSTQPPREADTODLDEVEGGAAPFNTRHSK 120
DB 61 ARVAGQTRNITVDPRLFKKRRLSPRVLPSTQPPREADTODLDEVEGGAAPFNTRHSK 120
QY 121 RSSSHPIFRGSESVCDVSVMVGDKTTATDIDKGEVWVLGEVINNSVFKQYFPETKCR 180
DB 121 RSSSHPIFRGSESVCDVSVMVGDKTTATDIDKGEVWVLGEVINNSVFKQYFPETKCR 180
QY 181 DPNPVDSCGRGIDSKHMSYCTTHTFVKALTMDSKQAAWRFIRIDTACVCLSRKAVRR 240
DB 181 DPNPVDSCGRGIDSKHMSYCTTHTFVKALTMDSKQAAWRFIRIDTACVCLSRKAVRR 240
QY 241 A 241
DB 241 A 241

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DB 241 A 241

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RESULT 3

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Q96P60 PRELIMINARY; PRT; 241 AA.
ID Q96P60
AC Q96P60
DT 01-DEC-2001 (TREMblrel. 19, Created)
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
DE Nerve growth factor beta.
GN NGFB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCB1_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RA Zhang Y., Zhang B., Zhou Y., Peng X., Yuan J., Qiang B.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF411526; AAL05874.1; -.
DR InterPro; IPR02072; NGF.
DR Pfam; PF00243; NGF.
DR Prodom; PD002052; NGF.
DR PROSITE; PS00248; NGF_1; UNKNOWN_1.
DR PROSITE; PS50270; NGF_2; 1.
SQ SEQUENCE 241 AA; 26964 MW; 745216485C21E558 CRC64;

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```

Query Match 99.1%; Score 1258; DB 4; Length 241;
Best Local Similarity 98.8%; Pred. No. 5.1e-116;
Matches 238; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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```

QY 1 MSMLFTTLTAFLIGIOAEPHSESNVPAAGHTIPQVWMTKQHSJLDTALRRASAPAAIA 60
DB 1 MSMLFTTLTAFLIGIOAEPHSESNVPAAGHTIPQVWMTKQHSJLDTALRRASAPAAIA 60
QY 61 ARVAGQTRNITVDPRLFKKRRLSPRVLPSTQPPREADTODLDEVEGGAAPFNTRHSK 120
DB 61 ARVAGQTRNITVDPRLFKKRRLSPRVLPSTQPPREADTODLDEVEGGAAPFNTRHSK 120
QY 121 RSSSHPIFRGSESVCDVSVMVGDKTTATDIDKGEVWVLGEVINNSVFKQYFPETKCR 180
DB 121 RSSSHPIFRGSESVCDVSVMVGDKTTATDIDKGEVWVLGEVINNSVFKQYFPETKCR 180
QY 181 DPNPVDSCGRGIDSKHMSYCTTHTFVKALTMDSKQAAWRFIRIDTACVCLSRKAVRR 240
DB 181 DPNPVDSCGRGIDSKHMSYCTTHTFVKALTMDSKQAAWRFIRIDTACVCLSRKAVRR 240
QY 241 A 241
DB 241 A 241

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RESULT 4

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Q9N2F0 PRELIMINARY; PRT; 241 AA.
ID Q9N2F0
AC Q9N2F0
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE Beta-nerve growth factor (Fragment).
GN Beta-NGF.
OS Gorilla gorilla (Gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Gorilla.
OX NCB1_TaxID=9593;
RN (1)
RP SEQUENCE FROM N.A.
RA STRAIN-GORILLA-UI;
RA Kltano T., Kobayakawa H., Saitou N.;
RT "Silver Project.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB037519; BAA90439.1; -.

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DR HSP; P01139; 1BET.
DR InterPro; IP002072; NGF.
DR Pfam; PF00243; NGF; 1.
DR PRINTS; PR00268; NGF.
DR ProDom; PD002052; NGF; 1.
DR SMART; SM00140; NGF; 1.
DR PROSITE; PS00248; NGF_1; 1.
DR PROSITE; PS00270; NGF_2; 1.
DR NON TER 241 241
SQ SEQUENCE 241 AA; 26915 MW; 6F5AD163C84B34 CRC64;

Query Match 98.3%; Score 1249; DB 6; Length 241;
Best Local Similarity 98.8%; Pred. No. 4e-115;
Matches 238; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MSMLFYTLITAFLLIGIOAEPHSESNVPAGHTIPQVHTKLOHSLDTALRRASAPAAIA 60
DB 1 MSMLFYTLITAFLLIGIOAEPHSESNVPAGHTIPQVHTKLOHSLDTALRRASAPAAIA 60
QY 61 ARVAGOTRNITVDPRLFKKRLRSPRVLFSTQPPREADTODLDFEVGAAPFNTRSK 120
DB 61 ARVAGOTRNITVDPRLFKKRLRSPRVLFSTQPPREADTODLDFEVGAAPFNTRSK 120
QY 121 RSSSHPIFRGFEFSCDSVSWVGDKTTATDIDKGEVWVLGEVINNSVFKQYFFETKCR 180
DB 121 RSSSHPIFRGFEFSCDSVSWVGDKTTATDIDKGEVWVLGEVINNSVFKQYFFETKCR 180
QY 181 DPNPVDGCGRIGDSKHNNSYCTTTHTFVKALTMGQKAAFRIRIDTACVCLSRKAVR 240
DB 181 DPNPVDGCGRIGDSKHNNSYCTTTHTFVKALTMGQKAAFRIRIDTACVCLSRKAVR 240
QY 241 A 241
DB 241 A 241

RESULT 5

Q9NZP1 PRELIMINARY; PRT; 241 AA.
AC Q9NZP1
DT 01-OCT-2000 (TRENBLrel. 15; Created)
DT 01-OCT-2000 (TRENBLrel. 15; Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19; Last annotation update)
DE Beta-nerve growth factor (Fragment).
GN BETA-NGF.
OS Pan troglodytes (Chimpanzee).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RC SEQUENCE FROM N.A.
RC STRAIN=CHIMP-220;
RA Kitano T., Kobayakawa H., Saitou N.,
RT "Silver Project."
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
EMBL; AB037518; BAA0438.1; -
DR HSP; P01139; 1BET.
DR InterPro; IP002072; NGF.
DR Pfam; PF00243; NGF; 1.
DR PRINTS; PR00268; NGF.
DR ProDom; PD002052; NGF; 1.
DR SMART; SM00140; NGF; 1.
DR PROSITE; PS00248; NGF_1; 1.
DR PROSITE; PS00270; NGF_2; 1.
DR NON TER 241 241
SQ SEQUENCE 241 AA; 26868 MW; B39FAA8912C00A0B CRC64;

Query Match 98.3%; Score 1248; DB 6; Length 241;
Best Local Similarity 98.3%; Pred. No. 5e-115;
Matches 237; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MSMLFYTLITAFLLIGIOAEPHSESNVPAGHTIPQVHTKLOHSLDTALRRASAPAAIA 60
DB 1 MSMLFYTLITAFLLIGIOAEPHSESNVPAGHTIPQVHTKLOHSLDTALRRASAPAAIA 60

DB 1 MSMLFYTLITAFLLIGIOAEPHSESNVPAGHTIPQVHTKLOHSLDTALRRASAPAAIA 60
QY 61 ARVAGOTRNITVDPRLFKKRLRSPRVLFSTQPPREADTODLDFEVGAAPFNTRSK 120
DB 61 ARVAGOTRNITVDPRLFKKRLRSPRVLFSTQPPREADTODLDFEVGAAPFNTRSK 120
QY 121 RSSSHPIFRGFEFSCDSVSWVGDKTTATDIDKGEVWVLGEVINNSVFKQYFFETKCR 180
DB 121 RSSSHPIFRGFEFSCDSVSWVGDKTTATDIDKGEVWVLGEVINNSVFKQYFFETKCR 180
QY 181 DPNPVDGCGRIGDSKHNNSYCTTTHTFVKALTMGQKAAFRIRIDTACVCLSRKAVR 240
DB 181 DPNPVDGCGRIGDSKHNNSYCTTTHTFVKALTMGQKAAFRIRIDTACVCLSRKAVR 240
QY 241 A 241
DB 241 A 241

RESULT 6

Q9NZB9 PRELIMINARY; PRT; 241 AA.
AC Q9NZB9
DT 01-OCT-2000 (TRENBLrel. 15; Created)
DT 01-OCT-2000 (TRENBLrel. 15; Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19; Last annotation update)
DE Beta-nerve growth factor (Fragment).
GN BETA-NGF.
OS Pongo pygmaeus (Orangutan).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pongo.
OX NCBI_TaxID=9600;
RN [1]
RC SEQUENCE FROM N.A.
RC STRAIN=ORAN-UI;
RA Kitano T., Kobayakawa H., Saitou N.,
RT "Silver Project."
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
EMBL; AB037520; BAA0440.1; -
DR HSP; P01139; 1BET.
DR InterPro; IP002072; NGF.
DR Pfam; PF00243; NGF; 1.
DR PRINTS; PR00268; NGF.
DR ProDom; PD002052; NGF; 1.
DR SMART; SM00140; NGF; 1.
DR PROSITE; PS00248; NGF_1; 1.
DR PROSITE; PS00270; NGF_2; 1.
DR NON TER 241 241
SQ SEQUENCE 241 AA; 26876 MW; DFC168E7E4E01F15 CRC64;

Query Match 98.2%; Score 1247; DB 6; Length 241;
Best Local Similarity 98.3%; Pred. No. 6.2e-115;
Matches 237; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MSMLFYTLITAFLLIGIOAEPHSESNVPAGHTIPQVHTKLOHSLDTALRRASAPAAIA 60
DB 1 MSMLFYTLITAFLLIGIOAEPHSESNVPAGHTIPQVHTKLOHSLDTALRRASAPAAIA 60
QY 61 ARVAGOTRNITVDPRLFKKRLRSPRVLFSTQPPREADTODLDFEVGAAPFNTRSK 120
DB 61 ARVAGOTRNITVDPRLFKKRLRSPRVLFSTQPPREADTODLDFEVGAAPFNTRSK 120
QY 121 RSSSHPIFRGFEFSCDSVSWVGDKTTATDIDKGEVWVLGEVINNSVFKQYFFETKCR 180
DB 121 RSSSHPIFRGFEFSCDSVSWVGDKTTATDIDKGEVWVLGEVINNSVFKQYFFETKCR 180
QY 181 DPNPVDGCGRIGDSKHNNSYCTTTHTFVKALTMGQKAAFRIRIDTACVCLSRKAVR 240
DB 181 DPNPVDGCGRIGDSKHNNSYCTTTHTFVKALTMGQKAAFRIRIDTACVCLSRKAVR 240
QY 241 A 241
DB 241 A 241

RESULT 7

09N183 PRELIMINARY; PRT; 217 AA.

AC 09N183; 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE Beta nerve growth factor (Fragment).
 OS Macaca fasciata (Japanese macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Macaca.
 NCBI_TaxID=9542;
 OX NCBI_TaxID=9542;
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RX MEDLINE=99270338; PubMed=10340513;
 RA Okuno H., Tokuyama W., Li Y.X., Hashimoto T., Miyashita Y.;
 RT "Quantitative evaluation of neurotrophin and trk mRNA expression in
 RT visual and limbic areas along the occipito-temporo-hippocampal pathway
 RT in adult macaque monkeys.";
 RL J. Comp. Neurol. 408:378-398 (1999).
 RN (2)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RA Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AF222662; AAF3790.1; -
 DR HSSP; P01139; 1BET.
 DR InterPro; IPR002072; NGF.
 DR Pfam; PF00243; NGF; 1.
 DR PRINTS; PR00268; NGF; 1.
 DR ProDom; PD002052; NGF; 1.
 DR SMART; SM00140; NGF; 1.
 DR PROSITE; PS00248; NGF_1; 1.
 DR PROSITE; PS50270; NGF_2; 1.
 FT NON_TER
 FT 1 217
 SQ SEQUENCE 217 AA; 24240 MW; 36A5A2D1DFCD8D5C CRC64;

Query Match 89.1%; Score 1132; DB 6; Length 217;
 Best Local Similarity 98.2%; Pred. No. 1.2e-103;
 Matches 213; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 11 APLIGIOAEPSSENVPAAGHTIPQVHTKLOHSIDTLRRRSAPAAIAARVAGQTRNI 70
 DB 1 APLIGIOAEPSSENVPAAGHTIPQVHTKLOHSIDTLRRRSAPAAIAARVAGQTRNI 60
 QY 71 TVDRLFKKRLRSFRLVSTOPREAADTODLFEVGAAPFRTTRSRSSSHPIFHR 130
 DB 61 TVDRLFKKRLRSFRLVSTOPREAADTODLFEVGAAPFRTTRSRSSSHPIFHR 120
 QY 131 GEFSVCDVSVMVDKTTATDIDKKEVMVLGEVINNSVFKQVFFETKCDPENVDSGCR 190
 DB 121 GEFSVCDVSVMVDKTTATDIDKKEVMVLGEVINNSVFKQVFFETKCDPENVDSGCR 180
 QY 191 GIDSKHNSYCTTHTTVKALVMDGKQAAFRIRIDT 227
 DB 181 GIDSKHNSYCTTHTTVKALVMDGKQAAFRIRIDT 217

RESULT 8

091XB4 PRELIMINARY; PRT; 294 AA.

AC 091XB4; 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE Similar to nerve growth factor, beta.
 GN NGFB.
 MS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Salivary Gland;
 RA Strauberg R.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC011123; AAI1123.1; -
 DR MGI; 97321; Ngfb.
 DR InterPro; IPR002072; NGF.
 DR Pfam; PF00243; NGF; 1.
 DR ProDom; PD002052; NGF; 1.
 DR PROSITE; PS00248; NGF_1; UNKNOWN_1.
 DR PROSITE; PS50270; NGF_2; 1.
 SQ SEQUENCE 294 AA; 32326 MW; 9EE7402DAC899229 CRC64;

Query Match 81.7%; Score 1038; DB 11; Length 294;
 Best Local Similarity 84.6%; Pred. No. 3.3e-94;
 Matches 193; Conservative 14; Mismatches 21; Indels 0; Gaps 0;

QY 1 MSMLFYTLTAPLIGIOAEPSSENVPAAGHTIPQVHTKLOHSIDTLRRRSAPAAIA 60
 DB 67 MSMLFYTLTAPLIGIOAEPSSENVPAAGHTIPQVHTKLOHSIDTLRRRSAPAAIA 126
 QY 61 ARVAGQTRNITVDPRLFKKRLRSFRLVSTOPREAADTODLFEVGAAPFRTTRSK 120
 DB 127 ARVAGQTRNITVDPRLFKKRLRSFRLVSTOPREAADTODLFEVGAAPFRTTRSK 186
 QY 121 RSSSHPIFHRGEFSVCDVSVMVDKTTATDIDKKEVMVLGEVINNSVFKQVFFETKCR 180
 DB 187 RSSSHPIFHRGEFSVCDVSVMVDKTTATDIDKKEVMVLGEVINNSVFKQVFFETKCR 246
 QY 181 DPNVPDSCGIDSKHNSYCTTHTTVKALVMDGKQAAFRIRIDT 228
 DB 247 ASNPVDSGCRGIDSKHNSYCTTHTTVKALVMDGKQAAFRIRIDT 294

RESULT 9

09DEZ9 PRELIMINARY; PRT; 241 AA.

AC 09DEZ9; 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE Nerve growth factor.
 OS Crotales durissus terrificus (South American rattlesnake).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosaurs; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Crotalus.
 NCBI_TaxID=8732;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=VENOM GLAND;
 RA Hayashi M.A.F., Radis-Baptista G., Yamane T., Camargo A.C.M.;
 RT "Cloning and sequence of a cDNA coding for a rattlesnake (Crotalus
 RT durissus terrificus) nerve growth factor.";
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF306533; AAG30924.1; -
 DR HSSP; P01139; 1BET.
 DR InterPro; IPR002072; NGF.
 DR Pfam; PF00243; NGF; 1.
 DR PRINTS; PR00268; NGF.
 DR ProDom; PD002052; NGF; 1.
 DR SMART; SM00140; NGF; 1.
 DR PROSITE; PS00248; NGF_1; 1.
 DR PROSITE; PS50270; NGF_2; 1.
 SQ SEQUENCE 241 AA; 27116 MW; 4A261F42C5D6F3F CRC64;

Query Match 56.1%; Score 713; DB 13; Length 241;
 Best Local Similarity 59.8%; Pred. No. 3e-62;
 Matches 144; Conservative 29; Mismatches 58; Indels 10; Gaps 4;

QY 1 MSMLFYTLITAFILIGIOAEPSHSESNYPAG---HTTPOVHTKLOHSIDTALRRASAPA 56
 DB 1 MSMLCTTLITLIIAFLIGIWAAPKSESNVPLSGPATSDLSDTSCATHALKTSHIIDOHYPA 60
 QY 57 AAIYA-RVAGQTRNTVDPPLFKKRLRSPRVLFSTOPPREADDTODLDEFGGAAPNR 115
 DB 61 PKKAEBOEFGSAAIIVDPKLFQKRRFQSPRVLFSTQPPPLSRDEQSV---DANSINR 116
 QY 116 THRSKSSSHPIFRHGEFVSCSVSWVWGDKTATDICKGEVNLGDEVNINNSVFKQYFF 175
 DB 117 NIRAAR-EDHPFKRGEYSVCSVNWVANKTATIDIGLVTWVWVNNNNVYKQYFF 175
 QY 176 ETKCRDPNVDGCRGIDSKHNSYCTTHTFYKALTMGQKQAAFPRIIDTACVCLSR 235
 DB 176 ETKCRPNVPVPGCRGIDARHNSYCTTNTFYKALTMESGNSMFPRIIDTACVCLSR 235
 QY 236 K 236
 DB 236 K 236

RESULT 10

Q90W38 PRELIMINARY; PRT; 241 AA.
 AC Q90W38;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Putative neurotrophic growth factor.
 GN NGF.
 OS Bothrops jararacussu (Jararacussu).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
 CC Viperidae; Crotalinae; Bothrops.
 NCBI_TaxID=8726;
 RX [1]
 RN SEQUENCE FROM N.A.
 RP TISSUE=VENOM GLAND;
 RA Kaashim S., Pereira J.O., Astolfi Filho S., Soares A.M.,
 RA Cintra A.C.O., Giglio J.R., Franca S.C.;
 RT "Molecular cloning and cDNA sequence of a nerve growth factor
 precursor from Bothrops jararacussu venomous gland."
 RL Submitted (AUG-2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AY007318; AAG12169.1;
 DR InterPro; IPR002072; NGF.
 DR Pfam; PF00243; NGF; 1.
 DR ProDom; PD002052; NGF; 1.
 DR PROSITE; PS00248; NGF_1; UNKNOWN_1.
 DR PROSITE; PS50270; NGF_2; 1.
 SQ SEQUENCE 241 AA; 27161 MW; AC57F724A6531A8F CRC64;

Query Match 55.8%; Score 709; DB 13; Length 241;
 Best Local Similarity 59.3%; Pred. No. 7.4e-62;
 Matches 143; Conservative 29; Mismatches 59; Indels 10; Gaps 4;

QY 1 MSMLFYTLITAFILIGIOAEPSHSESNYPAG---HTTPOVHTKLOHSIDTALRRASAPA 56
 DB 1 MSMLCTTLITLIIAFLIGIWAAPKSESNVPLSGPATSDLSDTSCATHALKTSHIIDOHYPA 60
 QY 57 AAIYA-RVAGQTRNTVDPPLFKKRLRSPRVLFSTOPPREADDTODLDEFGGAAPNR 115
 DB 61 PKKAEBOEFGSAAIIVDPKLFQKRRFQSPRVLFSTQPPPLSRDEQSV---DANSINR 116
 QY 116 THRSKSSSHPIFRHGEFVSCSVSWVWGDKTATDICKGEVNLGDEVNINNSVFKQYFF 175
 DB 117 NIRAAR-EDHPFKRGEYSVCSVNWVANKTATIDIGLVTWVWVNNNNVYKQYFF 175
 QY 176 ETKCRDPNVDGCRGIDSKHNSYCTTHTFYKALTMGQKQAAFPRIIDTACVCLSR 235
 DB 176 ETKCRPNVPVPGCRGIDARHNSYCTTNTFYKALTMESGNSMFPRIIDTACVCLSR 235
 QY 236 K 236

DB 236 K 236

RESULT 11

Q9PTC3 PRELIMINARY; PRT; 87 AA.
 AC Q9PTC3;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE Beta nerve growth factor (Fragment).
 GN NGF.
 OS Cervus elaphus scotticus.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae;
 CC Cervidae; Cervinae; Cervus.
 NCBI_TaxID=109627;
 RX [1]
 RN SEQUENCE FROM N.A.
 RP Robertson T.M., Stanton J.L., Clark D.E., Sheard P.W., Harris A.J.,
 RA Sutcliffe J.M.;
 RT "NGF expression in Antler."
 RL Submitted (Apr-1999) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AF145043; AAF17235.1;
 DR HSPF; P01139; IBET.
 DR InterPro; IPR002072; NGF.
 DR Pfam; PF00243; NGF; 1.
 DR PRINTS; PR00268; NGF.
 DR ProDom; PD002052; NGF; 1.
 DR SMART; SM00140; NGF; 1.
 DR PROSITE; PS00248; NGF_1; 1.
 DR PROSITE; PS50270; NGF_2; 1.
 FT NON TER 1
 FT NON TER 87
 SQ SEQUENCE 87 AA; 9876 MW; 17EB06B49AF7A0A4 CRC64;

Query Match 36.4%; Score 462; DB 6; Length 87;
 Best Local Similarity 96.6%; Pred. No. 4.7e-38;
 Matches 84; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 138 SVSWVWGDKTATDICKGEVNLGDEVNINNSVFKQYFFETKCRPNVPVPGCRGIDSKHNS 197
 DB 1 SVSWVWGDKTATDICKGEVNLGDEVNINNSVFKQYFFETKCRPNVPVPGCRGIDSKHNS 60
 QY 198 NSYCTTHTFYKALTMGQKQAAFPRIIDTACVCLSR 224
 DB 61 NSYCTTHTFYKALTMGQKQAAFPRIIDTACVCLSR 87

RESULT 12

Q9P2Z4 PRELIMINARY; PRT; 87 AA.
 AC Q9P2Z4;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Truncated beta nerve growth factor (Fragment).
 GN Homo sapiens (Human).
 OS Homo sapiens (Human).
 CC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 RX [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=95236507; PubMed=7720122;
 RA Li Y., Huang B., Cai L.;
 RT "Amplification, cloning and sequencing of beta nerve growth factor
 gene in the Chinese population."
 RL Chung-Kuo I Hsueh Ko Hsueh Yuan Hsueh Pao 16:334-338(1994).
 DR EMBL; S76884; AAB34114.2;
 DR HSPF; P01139; IBET.
 DR InterPro; IPR002072; NGF.
 DR Pfam; PF00243; NGF; 1.
 DR PRINTS; PR00268; NGF.

DR ProDom; PD002052; NGF; 1.
 DR SMART; SM00140; NGF; 1.
 DR PROSITE; PS50270; NGF_2; 1.
 FT NON TER
 SQ SEQUENCE 87 AA; 9729 MW; 45E9E27388FDEE27 CRC64;

Query Match
 Best Local Similarity 94.3%; Score 459; DB 4; Length 87;
 Matches 82; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 122 SSSHIIFRGEFVSDSVWVGDTTATDIDKGEVWMLGEVNNINSVFQYFETKCRD 181
 DB 1 SSSHIIFRGEFVSDSVWVGDTTATDIDKGEVWMLGEVNNINSVFQYFETKCRD 60
 QY 182 PNPVDSGCRGIDSKHMNSYCTTHTFV 208
 DB 61 PNPVDSGCRGIDSKHMNSYCTTHTFV 87

RESULT 13
 Q9WU15 PRELIMINARY; PRT; 132 AA.

DR 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Nerve growth factor (Fragment).
 OS Mesocricetus auratus (Golden hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Mesocricetus.
 NCBI_TaxID=10036;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Jansen H.T., Lehman M.N., Stevens P.J.;
 RT "Golden Hamster Neurotrophin and Neurotrophin Receptor cDNA."
 RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF104239; AAD21010.1; -
 FT NON TER
 FT NON TER
 SQ SEQUENCE 132 AA; 14649 MW; 0C36B6283225DA6 CRC64;

Query Match.
 Best Local Similarity 75.4%; Score 449.5; DB 11; Length 132;
 Matches 89; Conservative 10; Mismatches 18; Indels 1; Gaps 1;

QY 1 MSMLFYTLITAFPIGIAEPHSESNVPAHGTHIPVHTKIOHSLDIALRRASAPAAIA 60
 DB 16 MSMLFYTLITAFPIGIAEPHSESNVPAHGTHIPVHTKIOHSLDIALRRASAPAAIA 75
 QY 61 ARVAGOTRNTITVDPRLFKKRLSPRLPSTOPPREAADPDODFEVGAAPRRTR 118
 DB 76 ARVAGOTRNTITVDPRLFKKRLSPRLPSTOPPREAADPDODFEVGAAPRRTR 132

RESULT 14
 Q9N182 PRELIMINARY; PRT; 241 AA.

DR 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Neurotrophin-3 (Fragment).
 OS Macaca fasciata (Japanese macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Macaca.
 NCBI_TaxID=9542;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Gotz R., Koster R., Winkler C., Raulf F., Lottepeich F., Scharf M.,
 RX MEDLINE=99270338; PubMed=10340513;
 Okuno H., Tokuyama W., Li Y.X., Hashimoto T., Miyashita Y.;

RT "Quantitative evaluation of neurotrophin and trk mRNA expression in
 RT visual and limbic areas along the occipito-temporo-hippocampal pathway
 RT in adult macaque monkeys."
 RT J. Comp. Neurol. 408:378-398(1999).
 RN [2]

QY 4 LFTYTLITAFPIGIAEPHSESNVPAHGTHIPVHTKIOHSLDIALRRASAPAAIA 48
 DB 1 LFTYTLITAFPIGIAEPHSESNVPAHGTHIPVHTKIOHSLDIALRRASAPAAIA 60
 QY 49 RRA-----RSAPAAIAARVAGOTRNTITVDPRLFKKRLSPRLPSTOPPREAADT 100
 DB 61 PKAEPREPERGQPAKSEFPV-----IAMDTELRQGRVNSPRLVLSDSPLEPPPL 114
 QY 101 QDDFEVGAAPRRTRHRSKSSHPHFRGEVSDSVWVGDTTATDIDKGEVWML 160
 DB 115 YLMEEDYGNPVVANKRSRRKRYAEHK-SHREGVSDSVWVGDTTATDIDKGEVWML 173
 QY 161 GEVNNINSVFQYFETKCRDPNPVDSGCRGIDSKHMNSYCTTHTFVKTALYMD-GKQA 219
 DB 174 GEIKTNSVYKQFYTRCKEARPVNCGRGIDDKHMNSQCKTSQYVRLTSENKLVG 233
 QY 220 WRFIRIDT 227
 DB 234 WRFIRIDT 241

Query Match
 Best Local Similarity 33.6%; Score 426.5; DB 6; Length 241;
 Matches 97; Conservative 35; Mismatches 85; Indels 31; Gaps 6;

QY 4 LFTYTLITAFPIGIAEPHSESNVPAHGTHIPVHTKIOHSLDIALRRASAPAAIA 48
 DB 1 LFTYTLITAFPIGIAEPHSESNVPAHGTHIPVHTKIOHSLDIALRRASAPAAIA 60
 QY 49 RRA-----RSAPAAIAARVAGOTRNTITVDPRLFKKRLSPRLPSTOPPREAADT 100
 DB 61 PKAEPREPERGQPAKSEFPV-----IAMDTELRQGRVNSPRLVLSDSPLEPPPL 114
 QY 101 QDDFEVGAAPRRTRHRSKSSHPHFRGEVSDSVWVGDTTATDIDKGEVWML 160
 DB 115 YLMEEDYGNPVVANKRSRRKRYAEHK-SHREGVSDSVWVGDTTATDIDKGEVWML 173
 QY 161 GEVNNINSVFQYFETKCRDPNPVDSGCRGIDSKHMNSYCTTHTFVKTALYMD-GKQA 219
 DB 174 GEIKTNSVYKQFYTRCKEARPVNCGRGIDDKHMNSQCKTSQYVRLTSENKLVG 233
 QY 220 WRFIRIDT 227
 DB 234 WRFIRIDT 241

DR EMBL; L36326; AAA61921.1; -
 DR HSP; P01139; 1BET.
 DR InterPro; IPR002072; NGF.
 DR Pfam; PF00243; NGF; 1.
 DR PRINTS; PR00268; NGF.
 DR ProDom; PD002052; NGF; 1.
 DR SMART; SM00140; NGF; 1.
 DR PROSITE; PS00248; NGF; 1.
 DR PROSITE; PS50270; NGF_2; 1.
 DR Signal.
 KW SIGNAL.
 FT CHAIN 1 142
 FT SIGNAL 143 286
 SQ SEQUENCE 286 AA; 31424 MW; 5607DBA66792E12D CRC64;
 NEUROTROPHIN-6.
 Query Match 33.5%; Score 426; DB 13; Length 286;
 Best Local Similarity 38.6%; Pred. No. 7.5e-34;
 Matches 110; Conservative 31; Mismatches 84; Indels 60; Gaps 10;
 QY 8 LITAFLLIGIOAEPPHSESNV-----PAGHTIPQVH-----WTKLQHSIDTALRA 51
 Db 6 LVLLLLIGVQAVLNMGGLAARNPGAAHNSAGQETAAARGQLSODQTSYQOHRTHHRTK 65
 QY 52 RSAPAAA-----IAARVAGQT---RNIIVDPRLFKRRRLR-SPRVLFs--TOPPREAA 98
 Db 66 RTQSAASNMQNRTPVIGSPAGSSPDPSPVYDPKLFSGKHTRPSPRVFSSEVIPSHDVL 125
 QY 99 DTQDIDFE-VGGADPFNRTNTHRSKRSSSHPIFRGEPFVCDVSVMVGDKTTATDIDIKKEV 157
 Db 126 DGEGYDFERVRGL-----RVRRAVSHTHMRGEYSVCDsINTWV-NKTRATDMsGNEV 177
 QY 158 MYLGEVNIINNSVFQYFPETKCRD-----NEVDSGCRGIDSK 195
 Db 178 TVLSHVIVNNKVKQLFETTCRSPTHRSSGIVIGRSGGRGKGQSKTGNSGCRGIDSR 237
 QY 196 HNNSYCTTHTFEVKALTMDSKQAAWRFIRIDTACVCLSRKAVRR 240
 Db 238 YNNSCHTNTDIYSALIVFKEQTARFIRINACVCLSRNSWSR 282

Search completed: June 6, 2003, 10:50:56
 Job time : 29 secs

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OM protein - protein search, using sw model

Run on: June 6, 2003, 10:47:02 / Search time 9 Seconds
(without alignments)
1110.644 Million cell updates/sec

Title: US-09-788-188-1
Perfect score: 1270
Sequence: 1 MSMLFYTLITPAFLIGIOAEP.....FIRIDTACVCLSRKAVRA 241

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 112892 seqs, 41476328 residues
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	1270	100.0	241 1	NGF_HUMAN
2	1124	88.5	229 1	NGF_PIG
3	1107	87.2	241 1	NGF_BAT
4	1106	87.1	231 1	NGF_BOVIN
5	1096	86.3	241 1	NGF_MOUSE
6	1092	86.0	241 1	NGF_MOUSE
7	1073	84.5	241 1	NGF_PORC
8	788.5	62.1	243 1	NGF_PRANA
9	773	60.9	231 1	NGF_CHICK
10	675.5	53.2	243 1	NGF_XENLA
11	484	38.1	117 1	NGF_DABER
12	481.5	37.9	114 1	NGF_XIPWA
13	481.5	37.9	257 1	NT3_HUMAN
14	474	37.3	260 1	NT3_XENLA
15	473.5	37.3	257 1	NT3_PELCA
16	472	37.2	258 1	NT3_MOUSE
17	471.5	37.1	257 1	NT3_CHICK
18	471	37.1	258 1	NT3_RAT
19	459.5	36.2	233 1	NT7_BRABE
20	449.5	35.4	116 1	NGF_NAJNA
21	445.5	35.1	116 1	NGF_NAJNA
22	372.5	29.3	140 1	NT7_CYPCA
23	365	28.7	247 1	BDNF_HUMAN
24	364	28.7	249 1	BDNF_RAT
25	363	28.6	255 1	BDNF_CAVPO
26	362	28.5	247 1	BDNF_PROLO
27	361	28.4	247 1	BDNF_URSAR
28	361	28.4	247 1	BDNF_URSAR
29	360	28.3	249 1	BDNF_MOUSE
30	358.5	28.2	232 1	BDNF_PIG
31	350	27.6	247 1	BDNF_PELCA
32	348.5	27.4	248 1	BDNF_BOVIN
33	347.5	27.4	246 1	BDNF_CHICK

34	343	27.0	236 1	NT4_XENLA	P24727 xenopus lae
35	338.5	26.7	270 1	BDNF_CYPCA	O90322 cyprinus ca
36	337.5	26.6	210 1	NT5_HUMAN	P34130 homo sapien
37	335	26.4	269 1	BDNF_XIPWA	O02193 xiphophorus
38	330.5	26.0	209 1	NT5_RAT	P34131 rattus norv
39	323.5	25.5	114 1	BDNF_MACMU	O06225 macaca mla
40	307.5	24.2	114 1	BDNF_XENLA	P25432 xenopus lae
41	230	18.1	257 1	NT6B_HUMAN	P34133 homo sapien
42	227	17.9	257 1	NT6A_HUMAN	P34132 homo sapien
43	225	17.7	186 1	NT6G_HUMAN	P34134 homo sapien
44	190	15.0	42 1	NGF_VIPLE	P25428 vipera lebe
45	136	10.7	154 1	NT3_CEREL	O95150 cervus elap

ALIGNMENTS

RESULT 1
NGF_HUMAN STANDARD, PRT, 241 AA.
AC P01138;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Beta-nerve growth factor precursor (Beta-NGF).
GN NGFB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid:9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83244969; PubMed=668123;
RA Ullrich A., Gray A., Berman C., Dull T.J.;
RT "Human beta-nerve growth factor gene sequence highly homologous to
RL that of mouse.";
RL Nature 303:821-825(1983).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=84206565; PubMed=6327169;
RA Ullrich A., Gray A., Berman C., Coussens L., Dull T.J.;
RT "Sequence homology of human and mouse beta-NGF subunit genes.";
RL Cold Spring Harb. Symp. Quant. Biol. 48:435-442(1983).
RN [3]
RP SEQUENCE FROM N.A.
RX TISSUE=Brain;
RA Borsani G., Pizanti A., Rugarili E.I., Falini A., Silani V.,
RT "cDNA sequence of human beta-NGF.";
RL Nucleic Acids Res. 18:4020-4020(1990).
RN [4]
RP SEQUENCE OF 178-219 FROM N.A.
RX TISSUE=Leukocyte; PubMed=2025430;
RA Halboeck F., Ibanez C.F., Peterson H.;
RT "Evolutionary studies of the nerve growth factor family reveal a
RL novel member abundantly expressed in Xenopus ovary.";
RL Neuron 6:845-858(1991).
CC -I- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
CC MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT
CC STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
CC EMBRYONIC SENSORY NEURONS.
CC -I- SUBUNIT: HOMODIMER, ASSOCIATED BY NONCOVALENT FORCES.
CC -I- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
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CC EMBL; V01511; CA24755.1; -
DR EMBL; M21062; AA59931.1; -
DR EMBL; X52599; CA36832.1; -
DR PIR; A01399; NGRUBM.
DR PIR; S10253; S10253.
DR HSSP; P01139; 1BET.
DR Genew; HGNC; 7808; NGFB.
DR MIM; 162030; -
DR InterPro; IPR002072; NGF.
DR Pfam; PF00243; NGF; 1.
DR PRINTS; PR00268; NGF.
DR ProDom; PD002052; NGF; 1.
DR SMART; SM00140; NGF; 1.
DR PROSITE; PS00248; NGF_1; 1.
DR PROSITE; PS0270; NGF_2; 1.
DR Growth factor; Signal.
KW SIGNAL.
FT PROPEP.
FT CHAIN.
FT DISULFID.
FT DISULFID.
FT DISULFID.
FT CARBOHYD.
FT CARBOHYD.
SQ SEQUENCE 241 AA; 26987 MW; CFI84DC6B736B0F CRC64;

Query Match 100.0%; Score 1270; DB 1; Length 241;
Best Local Similarity 100.0%; Pred. No. 3e-113;
Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSMLFYTLITAFILGIGIAEPHSBSNVAGHTIPQVHNTKLOHSLDTRLRRASAPAAIA 60
DB 1 MSMLFYTLITAFILGIGIAEPHSBSNVAGHTIPQVHNTKLOHSLDTRLRRASAPAAIA 60
QY 61 ARVAGQRRNTVDPRLFKKRLSPRLFSTQPPREADTDODLFEVGAAPRRTRRSK 120
DB 61 ARVAGQRRNTVDPRLFKKRLSPRLFSTQPPREADTDODLFEVGAAPRRTRRSK 120
QY 121 RSSSHPIFRHGEFVSCDSVSWVGDKTATDIDIKGEVWVLGEVINNSVFKQFFETKCR 180
DB 121 RSSSHPIFRHGEFVSCDSVSWVGDKTATDIDIKGEVWVLGEVINNSVFKQFFETKCR 180
QY 121 RSSSHPIFRHGEFVSCDSVSWVGDKTATDIDIKGEVWVLGEVINNSVFKQFFETKCR 180
DB 121 RSSSHPIFRHGEFVSCDSVSWVGDKTATDIDIKGEVWVLGEVINNSVFKQFFETKCR 180
QY 181 DENPVDGCGIDSKMNSYCTTHTFVKALITMDGQAAMRFIRIDTACVLSRKAVER 240
DB 181 DENPVDGCGIDSKMNSYCTTHTFVKALITMDGQAAMRFIRIDTACVLSRKAVER 240
QY 241 A 241
DB 241 A 241

RESULT 2
NGF_PIG STANDARD; PRT; 229 AA.
ID NGF_PIG
AC Q29074;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DB Beta-nerve growth factor precursor (Beta-NGF) (Fragment).
GN NGFB.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_Taxid=9823;
(1)
RP SEQUENCE FROM N.A.
RC STRAIN=large white; TISSUE=Blood;
RX MEDLINE=94313891; PubMed=8039422;
RA Lab1b1d-nanals Y.; Mellink C.; Yeste M.; Gellin J.;
RT A new marker (NGFB) on pig chromosome 4, isolated by using a
RT consensus sequence conserved among species.
RL Cytogenet. Cell Genet. 67:120-125 (1994).

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CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
CC MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT
CC STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
CC EMBRYONIC SENSORY NEURONS.
CC -1- SUBUNIT: HOMODIMER, ASSOCIATED BY NONCOVALENT FORCES.
CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
CC
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CC
DR EMBL; L31898; AAA21301.1; -
DR HSSP; P01139; 1BET.
DR InterPro; IPR002072; NGF.
DR Pfam; PF00243; NGF; 1.
DR ProDom; PD002052; NGF; 1.
DR SMART; SM00140; NGF; 1.
DR PROSITE; PS00248; NGF_1; 1.
DR PROSITE; PS0270; NGF_2; 1.
DR Growth factor; Signal.
KW NON TER.
FT SIGNAL.
FT PROPEP.
FT CHAIN.
FT DISULFID.
FT DISULFID.
FT DISULFID.
FT CARBOHYD.
FT CARBOHYD.
SQ SEQUENCE 229 AA; 25275 MW; FE8890771CBA3189 CRC64;

Query Match 88.5%; Score 1124; DB 1; Length 229;
Best Local Similarity 92.6%; Pred. No. 2e-99;
Matches 212; Conservative 4; Mismatches 13; Indels 0; Gaps 0;

QY 13 LGIGIAEPHSBSNVAGHTIPQVHNTKLOHSLDTRLRRASAPAAIAARVAGQRRNTV 72
DB 1 LGIGIAEPHSBSNVAGHTIPQVHNTKLOHSLDTRLRRASAPAAIAARVAGQRRNTV 72
QY 1 LGIGIAEPHSBSNVAGHTIPQVHNTKLOHSLDTRLRRASAPAAIAARVAGQRRNTV 72
DB 1 LGIGIAEPHSBSNVAGHTIPQVHNTKLOHSLDTRLRRASAPAAIAARVAGQRRNTV 72
QY 73 DRLFKKRLSPRLFSTQPPREADTDODLFEVGAAPRRTRRSKSSHPFHRGE 132
DB 73 DRLFKKRLSPRLFSTQPPREADTDODLFEVGAAPRRTRRSKSSHPFHRGE 132
QY 61 DPKLFKKRLSPRLFSTQPPREADTDODLFEVGAAPRRTRRSKSSHPFHRGE 120
DB 61 DPKLFKKRLSPRLFSTQPPREADTDODLFEVGAAPRRTRRSKSSHPFHRGE 120
QY 133 FSVCDVSWVGDKTATDIDIKGEVWVLGEVINNSVFKQFFETKCRDPNPVDSGCGRI 192
DB 133 FSVCDVSWVGDKTATDIDIKGEVWVLGEVINNSVFKQFFETKCRDPNPVDSGCGRI 192
QY 121 FSVCDVSWVGDKTATDIDIKGEVWVLGEVINNSVFKQFFETKCRDPNPVDSGCGRI 180
DB 121 FSVCDVSWVGDKTATDIDIKGEVWVLGEVINNSVFKQFFETKCRDPNPVDSGCGRI 180
QY 181 DSKMNSYCTTHTFVKALITMDGQAAMRFIRIDTACVLSRKAVERA 241
DB 181 DSKMNSYCTTHTFVKALITMDGQAAMRFIRIDTACVLSRKAVERA 241

RESULT 3
NGF_PAT STANDARD; PRT; 241 AA.
ID NGF_PAT
AC P25427;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DB Beta-nerve growth factor precursor (Beta-NGF).
GN NGFB.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
(1)
RP SEQUENCE FROM N.A.
RX MEDLINE=89037223; PubMed=3184206;

```

RA Whittemore S.R., Friedman P.L., Lathammar D.G., Persson H.,
 RA Gonzalez-Carvajal M., Holets V.R.;
 RA "Rat beta-nerve growth factor sequence and site of synthesis in the
 RT adult hippocampus.";
 RL J. Neurosci. Res. 20:403-410 (1988).
 RN (2)
 RP SEQUENCE OF 178-219 FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Liver;
 RX MEDLINE=9122573; PubMed=2025430;
 RA Hallboeck F., Ibanez C.F., Persson H.;
 RA "Evolutionary studies of the nerve growth factor family reveal a
 RT novel member abundantly expressed in Xenopus ovary";
 RL Neuron 6:845-858 (1991).
 CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
 CC MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT
 CC STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
 CC EMBRYONIC SENSORY NEURONS.
 CC -1- SUBUNIT: HOMODIMER, ASSOCIATED BY NONCOVALENT FORCES.
 CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
 CC -----
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 CC -----
 CC EMBL; M36589; AAA1697.1; ALT_INIT.
 DR HSSP; P01139; 1BET.
 DR InterPro; IPR002072; NGF.
 DR Pfam; PF00243; NGF; 1.
 DR PRINTS; PR00268; NGF.
 DR PRODOM; PD002052; NGF; 1.
 DR SMART; SM00140; NGF; 1.
 DR PROSITE; PS00248; NGF_1; 1.
 DR PROSITE; PS50270; NGF_2; 1.
 KM Growth factor; Signal
 FT SIGNAL 1 18
 FT PROPEP 19 121 POTENTIAL.
 FT CHAIN 122 241 BETA-NERVE GROWTH FACTOR.
 FT DISULFID 136 201 BY SIMILARITY.
 FT DISULFID 179 229 BY SIMILARITY.
 FT DISULFID 189 231 BY SIMILARITY.
 FT CARBOHYD 69 69 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 114 114 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 166 166 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 241 AA; 27009 MW; 665F42371563213D CRC64;
 Query Match 87.2%; Score 1107; DB 1; Length 241;
 Best Local Similarity 85.8%; Pred. No. 8.7e-98;
 Matches 206; Conservative 14; Mismatches 20; Indels 0; Gaps 0;
 QY 1 MSMLFYTLIAFLIGIOAEPHSSNVPAGHTIPQVHWTKLOHSLDTLRARSPAAIA 60
 DB 1 MSMLFYTLIAFLIGIOAEPHSSNVPAGHTIPQVHWTKLOHSLDTLRARSPAAIA 60
 QY 61 ARVAGGQRTITVDRLEFKKRLKRLSPRLVFTSTQPREADTDLDPEVGAAPFNRTSRK 120
 DB 61 ARVAGGQRTITVDRLEFKKRLKRLSPRLVFTSTQPREADTDLDPEVGAAPFNRTSRK 120
 QY 121 RSSSHPIFHGSGSVCSVWVGDKTATDIDKKEKRWVZGAVVINSVRFQYFEFKR 180
 DB 121 RSSSHPIFHGSGSVCSVWVGDKTATDIDKKEKRWVZGAVVINSVRFQYFEFKR 180
 QY 181 DPNPVDGCGIGISKHNSTCTTHTFVKALITMDGKQAAFRIFIDTACVSRKAVR 240
 DB 181 DPNPVDGCGIGISKHNSTCTTHTFVKALITMDGKQAAFRIFIDTACVSRKAVR 240
 NGF_BOVIN STANDARD; PRT; 231 AA.

AC P13600; O18969;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Beta-nerve growth factor precursor (Beta-NGF) (Fragment).
 GN NGF.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OC NCB1_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RX MEDLINE=97430845; PubMed=9284944;
 RA Eldridge C., Laurent P., Hayes H., Rodellar C., Levezuel H.,
 RA Zaragosa P.;
 RT "Assignment of the beta-nerve growth factor (NGF) to bovine
 RL chromosome 3 band q23 by in situ hybridization.";
 RL Cytogenet. Cell Genet. 77:306-307 (1997).
 RN (2)
 RP SEQUENCE OF 107-231 FROM N.A.
 RX MEDLINE=8630647; PubMed=2427334;
 RA Meier R., Becker-Andre M., Gotz R., Heumann R., Shaw A., Thoenen H.;
 RT "Molecular cloning of bovine and chick nerve growth factor (NGF):
 RT delineation of conserved and unconserved domains and their
 RT relationship to the biological activity and antigenicity of NGF";
 RL EMBO J. 5:1489-1493 (1986).
 CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
 CC MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT
 CC STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
 CC EMBRYONIC SENSORY NEURONS.
 CC -1- SUBUNIT: HOMODIMER, ASSOCIATED BY NONCOVALENT FORCES.
 CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
 CC -----
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 CC -----
 CC EMBL; Y09566; CAAT0759.1; -
 DR EMBL; M26809; AAA30666.1; -
 DR PIR; A26312; A26312.
 DR HSSP; P01139; 1BET.
 DR InterPro; IPR002072; NGF.
 DR Pfam; PF00243; NGF; 1.
 DR PRODOM; PD002052; NGF; 1.
 DR SMART; SM00140; NGF; 1.
 DR PROSITE; PS00248; NGF_1; 1.
 DR PROSITE; PS50270; NGF_2; 1.
 KM Growth factor; Signal.
 FT NONTER 1 1
 FT SIGNAL 1 8
 FT PROPEP 9 111 POTENTIAL.
 FT CHAIN 112 231 BETA-NERVE GROWTH FACTOR.
 FT DISULFID 126 191 BY SIMILARITY.
 FT DISULFID 169 219 BY SIMILARITY.
 FT DISULFID 179 221 BY SIMILARITY.
 FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 118 118 L -> F (IN REF. 2).
 FT CONFLICT 161 161 R -> K (IN REF. 2).
 FT CONFLICT 230 231 AP -> RA (IN REF. 2).
 SQ SEQUENCE 231 AA; 25437 MW; 01605099291A418C CRC64;
 Query Match 87.1%; Score 1106; DB 1; Length 231;
 Best Local Similarity 90.7%; Pred. No. 1e-97;
 Matches 205; Conservative 7; Mismatches 14; Indels 0; Gaps 0;
 QY 11 APLIGIOAEPHSSNVPAGHTIPQVHWTKLOHSLDTLRARSPAAIAARVAGGQRTNI 70

DB 1 AFLIGIOAPHTESNVAPGAIIPAOWMIKLGHSIDTLVLRASAPAGPIAARVAGOTINI 60
 QY 71 TDPPLFKKRLRSRVLPSTQPPKADDTODLDFEVGAAPFNTHSKSSHPFHR 130
 DB 61 TDPPLFKKRLRSRVLPSTQPPKADDTODLDFEVGAAPFNTHSKSSHPFHR 120
 QY 131 GEFVSDSVYVGDKTATDCKGKXVNVIGVNNVFPQYFETKCRDPNPDSCGR 190
 DB 121 GEFVSDSVYVGDKTATDCKGKXVNVIGVNNVFPQYFETKCRDPNPDSCGR 180
 QY 191 GIDSXNNSYCTTHTFYKALTMDCQKQAMPRIRIDTACVCLSRK 236
 DB 181 GIDSXNNSYCTTHTFYKALTMDCQKQAMPRIRIDTACVCLSRK 226
 RESULT 5
 NGF_MOUSE STANDARD; PRT; 241 AA.
 AC P0139; Q63864;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DB Beta-nerve growth factor precursor (Beta-NGF).
 GN NGFB.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=83167518; PubMed=6336309;
 RA Scott J., Selby M.J., Urdas M.S., Quiroga M., Bell G.I., Rutter W.J.,
 RT "Isolation and nucleotide sequence of a cDNA encoding the precursor
 of mouse nerve growth factor.";
 RL Nature 302:538-540(1983).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=83244969; PubMed=6688123;
 RA Ullrich A., Gray A., Berman C., Dull T.J.,
 RT "Human beta-nerve growth factor gene sequence highly homologous to
 that of mouse.";
 RL Nature 303:821-825(1983).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=84206565; PubMed=6327169;
 RA Ullrich A., Gray A., Berman C., Coussens L., Dull T.J.,
 RT "Sequence homology of human and mouse beta-NGF subunit genes.";
 RL Cold Spring Harb. Symp. Quant. Biol. 48:435-442(1983).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX STRAIN=C57BL/6; TISSUE=Submaxillary gland;
 RA Selby M.J., Edwards R., Sharp F., Rutter W.J.,
 RT "Mouse nerve growth factor gene: structure and expression.";
 RL Mol. Cell. Biol. 7:3057-3064(1987).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93264918; PubMed=1284621;
 RA Yamamoto T., Yamakuni T., Okabe N., Amano T.,
 RT "Production and secretion of nerve growth factor by clonal striated
 muscle cell line, G8-1.";
 RL Neurochem. Int. 21:251-258(1992).
 RN [6]
 RP SEQUENCE OF 122-239.
 RX MEDLINE=73075048; PubMed=4566923;
 RA Angeletti R.H., Hermanson M.A., Bradshaw R.A.,
 RT "Amino acid sequences of mouse 2.5S nerve growth factor. II.
 Isolation and characterization of the thermolytic and peptic peptides
 and the complete covalent structure.";
 RL Biochemistry 12:1100-1115(1973).
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
 RX MEDLINE=92065986; PubMed=1956407;

RA McDonald N.O., Lapatto R., Murray-Rust J., Gunning J., Wlodawer A.,
 RA Blundell T.L.,
 RT "New protein fold revealed by a 2.3-A resolution crystal structure of
 RT nerve growth factor.";
 RL Nature 354:411-414(1991).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
 RX MEDLINE=94260545; PubMed=8201620;
 RA Holland D.R., Coussens L.S., Meng W., Matthews B.W.,
 RT "Nerve growth factor in different crystal forms displays structural
 RT flexibility and reveals zinc binding sites.";
 RL J. Mol. Biol. 239:385-400(1994).
 RN [9]
 RP X-RAY CRYSTALLOGRAPHY (3.15 ANGSTROMS) OF 7S COMPLEX.
 RC STRAIN=Swiss Webster; TISSUE=Submaxillary gland;
 RX MEDLINE=98035451; PubMed=9351801;
 RA Bax B., Blundell T.L., Murray-Rust J., McDonald N.O.,
 RT "Structure of mouse 7S NGF: a complex of nerve growth factor with
 RT four binding proteins.";
 RL Structure 5:1275-1285(1997).
 CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
 CC MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT
 CC STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
 CC EMBRYONIC SENSORY NEURONS.
 CC -1- SUBUNIT: HOMODIMER, ASSOCIATED BY NONCOVALENT FORCES.
 CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL, M35075; AAA39818.1; ALT_INIT.
 DR EMBL, V00836; CAA24221.1; ALT_INIT.
 DR EMBL, K01759; AAA39820.1; ALT_INIT.
 DR EMBL, M14805; AAA39821.1; ALT_INIT.
 DR EMBL, M17298; AAA37687.1; ALT_INIT.
 DR EMBL, M17296; AAA37687.1; JOINED.
 DR EMBL, M17297; AAA37687.1; JOINED.
 DR EMBL, S62089; CAB32081.2; ALT_SEQ.
 DR PIR, A01400; NGMSG.
 DR PDB, 1BET; 31-MAY-94.
 DR PDB, 1BFG; 08-MAR-96.
 DR PDB, 1SGF; 27-MAY-98.
 DR MGD, MGI:97321; NGFB.
 DR InterPro, IPR02072; NGF.
 DR Pfam, PF00243; NGF.1.
 DR PRINTS, PR00268; NGF.
 DR Prodom, PD002052; NGF.1.
 DR SMART, SM00140; NGF.1.
 DR PROSITE, PS00248; NGF_1; 1.
 DR PROSITE, PS50270; NGF_2; 1.
 DR PROSITE, PS50270; NGF_2; 1.
 KW Growth factor; Signal; 3D-structure.
 FT SIGNAL 1
 FT PROPEP 18
 FT CHAIN 122
 FT DISULFID 136
 FT DISULFID 179
 FT DISULFID 189
 FT CARBOHYD 69
 FT CARBOHYD 114
 FT CONFLICT 233
 FT SEQUENCE 241 AA; 27076 MW; 164465E1DC550081 CRC64;
 Query Match 86.3%; Score 1096; DB 1; Length 241;
 Best Local Similarity 85.0%; Pred. No. 9.6e-97;
 Matches 204; Conservative 14; Mismatches 22; Indels 0; Gaps 0;
 1 MSMPYITLPAFLIGQAPHTESNVAPGAIIPAOWMIKLGHSIDTLVLRASAPAGPIAARVAGOTINI 60

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Db      1 MSMLFTLITAFLLIGVQAEPTSDSNVPEGDSVPEAHMTKLQHSIDTALRRARSAPATAPIA 60
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Db      61 ARVAGOTRNITVDPRLLFKKRLRSRVLFTSTOPPREAADTODIDFVGAAPNRTRRSK 120
Qy      121 RSSHPHIFRGRSPVCDVSVMVGDKTATADIKGEVWVLGEVNNINSVFKQYFFETKCR 180
Db      121 RSSHPHIFRGRSPVCDVSVMVGDKTATADIKGEVWVLGEVNNINSVFKQYFFETKCR 180
Qy      121 RSSHPHIFRGRSPVCDVSVMVGDKTATADIKGEVWVLGEVNNINSVFKQYFFETKCR 180
Db      121 RSSHPHIFRGRSPVCDVSVMVGDKTATADIKGEVWVLGEVNNINSVFKQYFFETKCR 180
Qy      181 DNPVDSGCRGIDSGHNSYCTTHTFVKALTMDSQOAMRPIRIDTACVCLSRKAVR 240
Db      181 DNPVDSGCRGIDSGHNSYCTTHTFVKALTMDSQOAMRPIRIDTACVCLSRKAVR 240
Qy      181 DNPVDSGCRGIDSGHNSYCTTHTFVKALTMDSQOAMRPIRIDTACVCLSRKAVR 240
Db      181 DNPVDSGCRGIDSGHNSYCTTHTFVKALTMDSQOAMRPIRIDTACVCLSRKAVR 240

RESULT 6
NGF_CAVPO STANDARD; PRT; 241 AA.
AC P19093;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Beta-nerve growth factor precursor (Beta-NGF).
GN NGFB.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystericognathi; Cavidae; Cavia.
OC NCBI_TaxId=10141;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue=Prostate;
RX MEDLINE=89177243; PubMed=2926397;
RA Schwarz M.A., Fisher D., Bradshaw R.A., Isaacson P.J.;
RT "Isolation and sequence of a cDNA clone of beta-nerve growth factor
RL from the guinea pig prostate gland."
J. Neurochem. 52:1203-1209 (1989).
CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
CC MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT
CC STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
CC EMBRYONIC SENSORY NEURONS.
CC -1- SUBUNIT: HOMODIMER, ASSOCIATED BY NONCOVALENT FORCES.
CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
DR PIR, J10097; J10097.
DR HSSP; P01139; 1BET.
DR InterPro; IPR002072; NGF.
DR Pfam; PF00243; NGF; 1.
DR PRINTS; PR00268; NGF.
DR PRODOM; PD002052; NGF; 1.
DR SMART; SM00140; NGF; 1.
DR PROSITE; PS00248; NGF_1; 1.
DR PROSITE; PS50270; NGF_2; 1.
KW Growth factor; Signal.
FT SIGNAL 1
FT PROPEP 18
FT CHAIN 122
FT DISULFID 136
FT DISULFID 179
FT DISULFID 229
FT CARBOHYD 189
FT CARBOHYD 231
FT CARBOHYD 69
FT CARBOHYD 114
FT CARBOHYD 114
FT SEQUENCE 241 AA; 26821 MW; 2FAE26B197804BF4 CRC64;

Query Match 86.0%; Score 1092; DB 1; Length 241;
Best Local Similarity 86.2%; Pred. No. 2.3e-96;
Matches 207; Conservative 10; Mismatches 23; Indels 0; Gaps 0;
Qy      1 MSMLFTLITAFLLIGVQAEPTSDSNVPEGDSVPEAHMTKLQHSIDTALRRARSAPATAPIA 60
Db      1 MSMLFTLITAFLLIGVQAEPTSDSNVPEGDSVPEAHMTKLQHSIDTALRRARSAPATAPIA 60
Qy      61 ARVAGOTRNITVDPRLLFKKRLRSRVLFTSTOPPREAADTODIDFVGAAPNRTRRSK 120
Db      61 ARVAGOTRNITVDPRLLFKKRLRSRVLFTSTOPPREAADTODIDFVGAAPNRTRRSK 120
Qy      121 RSSHPHIFRGRSPVCDVSVMVGDKTATADIKGEVWVLGEVNNINSVFKQYFFETKCR 180
Db      121 RSSHPHIFRGRSPVCDVSVMVGDKTATADIKGEVWVLGEVNNINSVFKQYFFETKCR 180
Qy      121 RSSHPHIFRGRSPVCDVSVMVGDKTATADIKGEVWVLGEVNNINSVFKQYFFETKCR 180
Db      121 RSSHPHIFRGRSPVCDVSVMVGDKTATADIKGEVWVLGEVNNINSVFKQYFFETKCR 180
Qy      181 DNPVDSGCRGIDSGHNSYCTTHTFVKALTMDSQOAMRPIRIDTACVCLSRKAVR 240
Db      181 DNPVDSGCRGIDSGHNSYCTTHTFVKALTMDSQOAMRPIRIDTACVCLSRKAVR 240
Qy      181 DNPVDSGCRGIDSGHNSYCTTHTFVKALTMDSQOAMRPIRIDTACVCLSRKAVR 240
Db      181 DNPVDSGCRGIDSGHNSYCTTHTFVKALTMDSQOAMRPIRIDTACVCLSRKAVR 240

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Qy      121 RSSHPHIFRGRSPVCDVSVMVGDKTATADIKGEVWVLGEVNNINSVFKQYFFETKCR 180
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Db      121 RSSHPHIFRGRSPVCDVSVMVGDKTATADIKGEVWVLGEVNNINSVFKQYFFETKCR 180
Qy      181 DNPVDSGCRGIDSGHNSYCTTHTFVKALTMDSQOAMRPIRIDTACVCLSRKAVR 240
Db      181 DNPVDSGCRGIDSGHNSYCTTHTFVKALTMDSQOAMRPIRIDTACVCLSRKAVR 240
Qy      181 DNPVDSGCRGIDSGHNSYCTTHTFVKALTMDSQOAMRPIRIDTACVCLSRKAVR 240
Db      181 DNPVDSGCRGIDSGHNSYCTTHTFVKALTMDSQOAMRPIRIDTACVCLSRKAVR 240

RESULT 7
NGF_PRANA STANDARD; PRT; 241 AA.
AC P20675;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Beta-nerve growth factor precursor (beta-NGF).
GN NGFB.
OS Praomys natalensis (African soft-furred rat) (Mastomys natalensis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
OC Mastomys.
OC NCBI_TaxId=10112;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=89172070; PubMed=3234767;
RA Fahnestock M., Bell R.A.;
RT "Molecular cloning of a cDNA encoding the nerve growth factor
RL precursor from Mastomys natalensis."
Gene 63:257-264 (1988).
CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
CC MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT
CC STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
CC EMBRYONIC SENSORY NEURONS.
CC -1- SUBUNIT: HOMODIMER, ASSOCIATED BY NONCOVALENT FORCES.
CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
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CC -----
DR EMBL; M22748; AAA40599.1; ALT_INT.
DR PIR; J03433; NGRTBA.
DR HSSP; P01139; 1BETG.
DR InterPro; IPR002072; NGF.
DR Pfam; PF00243; NGF; 1.
DR PRINTS; PR00268; NGF.
DR PRODOM; PD002052; NGF; 1.
DR SMART; SM00140; NGF; 1.
DR PROSITE; PS00248; NGF_1; 1.
DR PROSITE; PS50270; NGF_2; 1.
KW Growth factor; Signal.
FT SIGNAL 1
FT PROPEP 18
FT CHAIN 122
FT DISULFID 136
FT DISULFID 179
FT DISULFID 229
FT CARBOHYD 189
FT CARBOHYD 231
FT CARBOHYD 69
FT CARBOHYD 114
FT CARBOHYD 114
FT SEQUENCE 241 AA; 27035 MW; 8BFB207A1FEB2F7 CRC64;

Query Match 84.5%; Score 1073; DB 1; Length 241;
Best Local Similarity 83.3%; Pred. No. 1.5e-94;
Matches 200; Conservative 17; Mismatches 23; Indels 0; Gaps 0;
Qy      1 MSMLFTLITAFLLIGVQAEPTSDSNVPEGDSVPEAHMTKLQHSIDTALRRARSAPATAPIA 60
Db      1 MSMLFTLITAFLLIGVQAEPTSDSNVPEGDSVPEAHMTKLQHSIDTALRRARSAPATAPIA 60
Qy      61 ARVAGOTRNITVDPRLLFKKRLRSRVLFTSTOPPREAADTODIDFVGAAPNRTRRSK 120
Db      61 ARVAGOTRNITVDPRLLFKKRLRSRVLFTSTOPPREAADTODIDFVGAAPNRTRRSK 120
Qy      121 RSSHPHIFRGRSPVCDVSVMVGDKTATADIKGEVWVLGEVNNINSVFKQYFFETKCR 180
Db      121 RSSHPHIFRGRSPVCDVSVMVGDKTATADIKGEVWVLGEVNNINSVFKQYFFETKCR 180
Qy      121 RSSHPHIFRGRSPVCDVSVMVGDKTATADIKGEVWVLGEVNNINSVFKQYFFETKCR 180
Db      121 RSSHPHIFRGRSPVCDVSVMVGDKTATADIKGEVWVLGEVNNINSVFKQYFFETKCR 180
Qy      181 DNPVDSGCRGIDSGHNSYCTTHTFVKALTMDSQOAMRPIRIDTACVCLSRKAVR 240
Db      181 DNPVDSGCRGIDSGHNSYCTTHTFVKALTMDSQOAMRPIRIDTACVCLSRKAVR 240
Qy      181 DNPVDSGCRGIDSGHNSYCTTHTFVKALTMDSQOAMRPIRIDTACVCLSRKAVR 240
Db      181 DNPVDSGCRGIDSGHNSYCTTHTFVKALTMDSQOAMRPIRIDTACVCLSRKAVR 240

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Db 1 MSMLFTLITALLIGVQAPYDSDNPEBDSVPEANWTLQHSIDTLRALRRASAPAPA 60
Qy 61 ARVAGGTNTITDPLFKGRRLSPVLFSTOPPREADTODLDFEVGGAAPNTRTSK 120
Db 61 ARVAGGTNTITDPLFKGRRLSPVLFSTOPPREADTODLDFEVGGAAPNTRTSK 120
Qy 121 RSSSHDIFRGESEVDSVSWVGDKTATDICKGEVWVLGEVININNSFKQYFETKCR 180
Db 121 RSSSHDIFRGESEVDSVSWVGDKTATDICKGEVWVLGEVININNSFKQYFETKCR 180
Qy 181 DPNPVDGCGRIDSKMNSYCTTHTFVKTALTMGKQAMRFIRIDTACVLSKAVR 240
Db 181 ANNPVSGCGRIDSKMNSYCTTHTFVKTALTMGKQAMRFIRIDTACVLSKAVR 240

RESULT 8
NGF CHICK STANDARD; PRT; 243 AA.
AC P05200;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DB Beta-nerve growth factor precursor (Beta-NGF).
GN NGFB.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN 1;
RP SEQUENCE FROM N.A.
RX MEDLINE=86300546; PubMed=3017695;
RA Ebdendahl T., Larhammar D., Persson H.;
RT "Structure and expression of the chicken beta nerve growth factor
RT gene.";
RL EMO J. 5:1483-1487(1986).
RN 2;
RP SEQUENCE OF 118-243 FROM N.A.
RX MEDLINE=86248129; PubMed=3720959;
RA Wilson D., Perret C., Frechin N., Keller A., Behar G., Brachet P.,
RA Auffray C.;
RT "Molecular cloning of the avian beta-nerve growth factor gene:
RT transcription in brain.";
RL FEBS Lett. 203:82-86(1986).
RN 3;
RP SEQUENCE OF 121-243 FROM N.A.
RX MEDLINE=86300647; PubMed=2427334;
RA Meier R., Becker-Andre M., Gotz R., Heumann R., Shaw A., Thoenen H.;
RT "Molecular cloning of bovine and chick nerve growth factor (NGF):
RT delineation of conserved and unconserved domains and their
RT relationship to the biological activity and antigenicity of NGF.";
RL EMO J. 5:1489-1493(1986).
RN 4;
RP SEQUENCE OF 181-222 FROM N.A.
RX MEDLINE=91223573; PubMed=2025430;
RA Hallboeck F., Ibanez C.F., Persson H.;
RT "Evolutionary studies of the nerve growth factor family reveal a
RT novel member abundantly expressed in Xenopus ovary.";
RL Neuron 6:845-858(1991).
CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
CC MAINTENANCE OF THE SYMPATHETIC AND SENSORY NEURONS. IT
CC STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
CC EMBRYONIC SENSORY NEURONS.
CC -1- SUBUNIT: HOMODIMER, ASSOCIATED BY NONCOVALENT FORCES.
CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
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CC -----
DR EMBL; X04003; CAA27633.1; ALT_INIT.
DR EMBL; X04067; CAA27703.1; -.
DR EMBL; M26810; AAA48984.1; -.
DR PIR; A24857; A24857.
DR PIR; A26311; A26311.
DR HSSP; P01139; 1BET.
DR InterPro; IPR002072; NGF.
DR Pfam; PF00243; NGF; 1.
DR PRINTS; PR00268; NGF.
DR PRODOM; PD002052; NGF; 1.
DR SMART; SM00140; NGF; 1.
DR PROSITE; PS00248; NGF; 1; 1.
DR PROSITE; PS0270; NGF; 2; 1.
KM Growth factor; Signal.
FT SIGNAL.
FT PROPEP 23 125
FT CHAIN 126 243
FT DISULFD 139 204
FT DISULFD 182 232
FT DISULFD 192 234
SQ SEQUENCE 243 AA; 27138 MW; 74C306CB2079DA07 CRC64;

Query Match 62.1%; Score 788.5; DB 1; Length 243;
Best Local Similarity 64.9%; Pred. No. 1,46-67;
Matches 161; Conservative 20; Mismatches 48; Indels 19; Gaps 6;

Qy 1 MSMLFTLITAFILIGVQAPYDSDNPEBDSVPEANWTLQHSIDTLRALRRASAPA 56
Db 5 MSMLFTLITAFILIGVQAPYDSDNPEBDSVPEANWTLQHSIDTLRALRRASAPA 57
Qy 57 AATAARVA-----GQNTITVDPRLFKGRRLSPVLFSTOPPREADTODLDFEVGGA 111
Db 58 TT-HGRAMPDGDIEDINIMDQNFKKRFRSRVLFTOPPVSKGSGTF-LSSAV 115
Qy 112 PPNRTRSKSSSHPIFRGESEVDSVSWVGDKTATDICKGEVWVLGEVININNSVFK 171
Db 116 SLNRIRATKTA-TAPVLAHGEFVDSVSWVGDKTATDICKGEVWVLGEVININNSVFK 174
Qy 172 QYFEFKCRPNVVDGCGRIDSKMNSYCTTHTFVKTALTMGKQAMRFIRIDTACVC 231
Db 175 QYFEFKCRPNVVDGCGRIDSKMNSYCTTHTFVKTALTMGKQAMRFIRIDTACVC 234
Qy 232 VLSRKAVR 239
Db 235 VLSRKSGR 242

RESULT 9
NGF XENLA STANDARD; PRT; 231 AA.
AC P1617;
DT 01-MAY-1991 (Rel. 18, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Nerve growth factor precursor (NGF).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodidae; Xenopus.
OX NCBI_TaxID=8355;
RN 1;
RP SEQUENCE FROM N.A.
RX MEDLINE=91362944; PubMed=1888511;
RA Carriero F., Campion M., Cardinali B., Pierandrei-Amaldi P.;
RT "Structure and expression of the nerve growth factor gene in Xenopus
RT oocytes and embryos.";
RL Mol. Reprod. Dev. 29:313-322(1991).
RN 2;
RP SEQUENCE OF 170-211 FROM N.A.
RX TISSUE-Liver;
RX MEDLINE=91222573; PubMed=2025430;

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RA Halboeck F., Ibanez C.F., Persson H.;
 RT "Evolutionary studies of the nerve growth factor family reveal a
 RL novel member abundantly expressed in Xenopus ovary.";
 CC Neuron 6:845-858(1991).
 CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
 CC MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT
 CC STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
 CC SYMPATHETIC SENSORY NEURONS.
 CC -1- SUBUNIT: HOMODIMER, ASSOCIATED BY NONCOVALENT FORCES.
 CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
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 CC -----
 CC EMBL, X55716, CAA39249.1, ALT_INIT.
 CC PIR, S1481, S1481.
 CC HSSP, P01139, 1BET.
 CC InterPro, IPR002072, NGF.
 CC Pfam, PF00243, NGF, 1.
 CC PRINTS, PR00268, NGF.
 CC ProDom, PD002052, NGF, 1.
 CC SMART, SM00140, NGF, 1.
 CC PROSITE, PS00248, NGF, 1, 1.
 CC PROSITE, PS0270, NGF_2, 1.
 CC Growth factor, signal.
 CC KW SIGNAL, 1, 18
 CC FT PROPER, 19, 114 POTENTIAL.
 CC FT CHAIN, 115, 231 NERVE GROWTH FACTOR.
 CC FT DISULFID, 128, 193 BY SIMILARITY.
 CC FT DISULFID, 171, 221 BY SIMILARITY.
 CC FT DISULFID, 181, 223 BY SIMILARITY.
 CC FT CARBOHYD, 63, 63 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD, 107, 107 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD, 158, 158 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC SEQUENCE 231 AA; 26416 MW; 72A04E7D00B858C5 CRC64;
 SQ
 Query Match 60.9%; Score 773; DB 1; Length 231;
 Best Local Similarity 63.6%; Pred. No. 3.9e-66;
 Matches 154; Conservative 27; Mismatches 41; Indels 20; Gaps 6;
 QY 1 MSMLFTLTITLFLIGIOAEPHSNSVPAQHT---IP-QVHWTK-LQHSIDTALRRASAA 54
 DB 1 MSMLFTLTITLILISVQAAPKTKDHPARSSAKSRIPHTHTKSLHNS----- 49
 QY 55 PAAAIARVAQOTRNTVDPRLFKKRLRSPRVLPSTOPPRAADTODLDFEVGAAPFN 114
 DB 50 -HGLEAKPEPFFRNVTVDPKLFRKRPSPRVLPSTOPPRLSEDFQHLLEY-LDDEBSLN 107
 QY 115 RTHSKSSSHPIFRHGFSPVCDISVWVGDKTTATDJKGEVWVLGEVNNINSVFKQYF 174
 DB 108 KTRAKA-TYAPVHKKEYISVCDISVWVGDKTTATDJKGEVWVLGEVNNINSVFKQYF 166
 QY 175 FETCRDPNPVDSGGRGIDSKRWNSYCTTHTFYVALTMDGKQAAWRIRIDTACVLSR 234
 DB 167 FETCRDPNPVDSGGRGIDSKRWNSYCTTHTFYVALTMDGKQAAWRIRIDTACVLSR 226
 QY 235 RK 236
 DB 227 RK 228
 RESULT 10
 ID NGF_BUNMU STANDARD; PRT; 243 AA.
 AC P34128;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Nerve growth factor precursor (NGF).
 OS Bungarus multicinctus (Many-banded krait).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Elapidae; Bungarinae; Bungarus.
 CC NCBI_Taxid=8616;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Venom gland;
 RX MEDLINE=93192074; PubMed=7916740;
 RA Danse J.M., Garnier J.M.;
 RT "Molecular cloning of a cDNA encoding a nerve growth factor precursor
 from the krait, Bungarus multicinctus.";
 RL Growth Factors 8:77-86(1993).
 CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
 CC MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT
 CC STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
 CC SYMPATHETIC SENSORY NEURONS AS WELL AS BASAL FOREBRAIN CHOLINERGIC
 CC NEURONS IN THE BRAIN.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
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 CC EMBL, S56212, AAB25729.1, -
 CC HSSP, P01139, 1BET.
 CC InterPro, IPR002072, NGF.
 CC Pfam, PF00243, NGF, 1.
 CC PRINTS, PR00268, NGF.
 CC ProDom, PD002052, NGF, 1.
 CC SMART, SM00140, NGF, 1.
 CC PROSITE, PS00248, NGF, 1, 1.
 CC PROSITE, PS0270, NGF_2, 1.
 CC Growth factor, signal.
 CC KW SIGNAL, 1, 18 POTENTIAL.
 CC FT PROPER, 19, 125 NERVE GROWTH FACTOR.
 CC FT CHAIN, 126, 243 BY SIMILARITY.
 CC FT DISULFID, 139, 204 BY SIMILARITY.
 CC FT DISULFID, 182, 232 BY SIMILARITY.
 CC FT DISULFID, 192, 234 BY SIMILARITY.
 CC SEQUENCE 243 AA; 27514 MW; E33F64B142179A08 CRC64;
 SQ
 Query Match 53.2%; Score 675.5; DB 1; Length 243;
 Best Local Similarity 56.8%; Pred. No. 7.3e-57;
 Matches 137; Conservative 30; Mismatches 67; Indels 7; Gaps 4;
 QY 1 MSMLFTLTITLFLIGIOAEPHSNSVPAQHT---HTIQVHWTKLQHSIDTALRRASAA 56
 DB 1 MSMLFTLTITLILISVQAAPKTKDHPARSSAKSRIPHTHTKSLHNS----- 49
 QY 57 AAIARVAQOTRNTVDPRLFKKRLRSPRVLPSTOPPRAADTODLDFEVGAAPFN 115
 DB 61 PKESDDELGAANITVDPKLFRKRPSPRVLPSTOPPRLSEDFQHLLEY-LDDEBSLN 119
 QY 116 THRKRSSSHPIFRHGFSPVCDISVWVGDKTTATDJKGEVWVLGEVNNINSVFKQYF 175
 DB 120 NIMA-NMENHVNHGSHSVCDISVWVGDKTTATDJKGEVWVLGEVNNINSVFKQYF 178
 QY 176 FETCRDPNPVDSGGRGIDSKRWNSYCTTHTFYVALTMDGKQAAWRIRIDTACVLSR 235
 DB 179 FETCRDPNPVDSGGRGIDSKRWNSYCTTHTFYVALTMDGKQAAWRIRIDTACVLSR 238
 QY 236 K 236
 DB 239 K 239

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RESULT 11
NGF_DABRR STANDARD; PRT; 117 AA.
AC P30594;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Nerve growth factor (NGF)
OS Daboia russelli russelli (Russell's viper) (Vipera russelli russelli)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Viperidae; Viperinae; Daboia.
OX NCBI_TaxID=31159;
RN [1]
RP SEQUENCE.
RC TISUB=Venom;
RX MEDLINE=93120151; PubMed=1477101;
RA Koyama J.-I., Inoue S., Ikeda K., Hayashi K.;
RT "Purification and amino-acid sequence of a nerve growth factor from
RT the venom of Vipera russelli russelli."
RL Biochim. Biophys. Acta 1160:287-292(1992).
CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
CC MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT
CC STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
CC EMBRYONIC SENSORY NEURONS AS WELL AS BASAL FOREBRAIN CHOLINERGIC
CC NEURONS IN THE BRAIN.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
DR HSSP; P01139; 1BET.
DR InterPro; IPR002072; NGF.
DR Pfam; PF00243; NGF.1.
DR PRINTS; PR00268; NGF.
DR PRODOM; PD002052; NGF.1.
DR SMART; SM00140; NGF.1.
DR PROSITE; PS00248; NGF.1; 1.
DR PROSITE; PS50270; NGF.2; 1.
KW Glycoprotein; Growth Factor.
FT DISULFID 12 77
FT DISULFID 55 105
FT DISULFID 65 107
FT CARBOHYD 21 21
SQ SEQUENCE 117 AA; 13283 MW; A64559CSEPCIF66 CRC64;

Query Match 38.1%; Score 484; DB 1; Length 117;
Best Local Similarity 74.1%; Pred. No. 4,4e-39;
Matches 83; Conservative 19; Mismatches 10; Indels 0; Gaps 0;

QY 125 HP1FHRGFSVSVWVGDKTATD1KKEVAVLGEVNNINSVFQYFFETKCRDNP 184
DB 1 HPVHNOGEFSVCSVSVAANKTAT1MRGAVTVWVDVNLNNVYKQYFFETKCRNPNP 60

QY 185 VDSGCRGIDSKHNSYCTTHTFVKALTMDSKQAMRFIRIDTACVCLSKA 236
DB 61 VPSGCRGIDAKHNSYCTTIDTFRALTMERNQASMRFININACVCLSK 112

RESULT 12
NGF_XIPMA STANDARD; PRT; 194 AA.
AC P34129;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-OCT-2001 (Rel. 40, Last annotation update)
DE Nerve growth factor precursor (NGF).
OS Xiphophorus maculatus (Southern platyfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Petcomorpha; Atherinomorpha;
OC Cyprinodontiformes; Poeciliidae; Xiphophorus.
OX NCBI_TaxID=8083;
RN [1]
RP SEQUENCE FROM N.A.

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RX MEDLINE=92333301; PubMed=1629719;
RA Gotz R., Raulf F., Scharl M.;
RT "Brain-derived neurotrophic factor is more highly conserved in
RT structure and function than nerve growth factor during vertebrate
RT evolution."
RL J. Neurochem. 59:432-442(1992).
CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
CC MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT
CC STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
CC EMBRYONIC SENSORY NEURONS AS WELL AS BASAL FOREBRAIN CHOLINERGIC
CC NEURONS IN THE BRAIN.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
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CC -----
DR EMBL; X59941; CA442566.1; -
DR HSSP; P01139; 1BET.
DR InterPro; IPR002072; NGF.
DR Pfam; PF00243; NGF.1.
DR PRINTS; PR00268; NGF.
DR PRODOM; PD002052; NGF.1.
DR SMART; SM00140; NGF.1.
DR PROSITE; PS00248; NGF.1; FALSE_NEG.
DR PROSITE; PS50270; NGF.2; 1.
KW Growth factor; Signal.
FT SIGNAL 1 30
FT PROPEP 31 79
FT CHAIN 80 194
FT DISULFID 90 155
FT DISULFID 133 183
FT DISULFID 143 185
SQ SEQUENCE 194 AA; 21596 MW; 0369E0FA51147AE CRC64;

Query Match 37.9%; Score 481.5; DB 1; Length 194;
Best Local Similarity 58.9%; Pred. No. 1,4e-38;
Matches 99; Conservative 13; Mismatches 39; Indels 17; Gaps 3;

QY 71 TVDPRLFKRRRLSPVLFSTOPEAREADTDQDFE-VGGAAPFNRTHSKSSHP1FH 129
DB 40 TVDPRLFKRRRLSPVLFSSQPP-----DAEPAGQGVSRTRRQPPQ-----H 83

QY 130 RGEFSVCSVSVAWVGDKTATD1KKEVAVLGEVNNINSVFQYFFETKCRDNPVDSGC 189
DB 84 RGVYSVCSVSVAWVGNKTATD1SGKEVTVLPVNNINNVKKQYFFETTHSPSPSGSRC 143

QY 190 RIGDSKHNNSYCTTHTFVKALTMDSKQAMRFIRIDTACVCLSKA 237
DB 144 LGIDAHNNSHCTNSHTFVRALTSSENQVAMRLIRINACVCLSKS 191

RESULT 13
NT3_HUMAN STANDARD; PRT; 257 AA.
AC P20783;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Neurotrophin-3 precursor (NT-3) (Neurotrophic factor) (HDNF)
OS (Nerve growth factor 2) (NGF-2).
GN NTF3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

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RA MEDLINE=90262727; PubMed=2344409;
 RA Rosenthal A., Goeddel D.V., Nguyen T., Lewis M., Shih A.,
 RA Laramee G.R., Nikolic K., Winslow J.W.,
 RA "Primary structure and biological activity of a novel human
 RT neurotrophic factor.";
 RL Neuron 4:767-773 (1990).
 [2]
 RP SEQUENCE FROM N.A.
 RP MEDLINE=91045937; PubMed=2236018;
 RA Jones K.R., Reichardt L.F.,
 RA "Molecular cloning of a human gene that is a member of the nerve
 RT growth factor family.";
 RT Proc. Natl. Acad. Sci. U.S.A. 87:8060-8064 (1990).
 [3]
 RP SEQUENCE FROM N.A.
 RP MEDLINE=90306351; PubMed=2365067;
 RA Kishino Y., Yoshimura K., Nakahama K.,
 RA "Cloning and expression of a cDNA encoding a novel human neurotrophic
 RT factor.";
 RT FEBS Lett. 266:187-191 (1990).
 [4]
 RP SEQUENCE FROM N.A.
 RP MEDLINE=91365361; PubMed=1869806;
 RA Maisongrange P.C., le Beau M.M., Espinosa R. III, Ip N.Y.,
 RA Belluscio L., de la Monte S.M., Squinto S., Furch M.E.,
 RA Yancopoulos G.D.,
 RA "Human and rat brain-derived neurotrophic factor and neurotrophin-3:
 RT gene structures, distributions, and chromosomal localizations.";
 RT Genomics 10:558-568 (1991).
 [5]
 RP SEQUENCE OF 194-236 FROM N.A.
 RP TISSUE=Leukocyte;
 RP MEDLINE=91222573; PubMed=2025430;
 RA Hallboeck F., Ibanez C.F., Persson H.,
 RA "Evolutionary studies of the nerve growth factor family reveal a
 RT novel member abundantly expressed in Xenopus ovary.";
 RT Neuron 6:845-858 (1991).
 [6]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
 RP MEDLINE=95217877; PubMed=7703225;
 RA Robinson R.C., Radziejewski C., Stuart D.I., Jones E.Y.,
 RA "Structure of the brain-derived neurotrophic factor/neurotrophin 3
 RT heterodimer.";
 RL Biochemistry 34:4139-4146 (1995).
 [7]
 RP VARIANT GLU-76.
 RP MEDLINE=95251647; PubMed=7733919;
 RA Hattori M., Nanko S.,
 RA "Association of neurotrophin-3 gene variant with severe forms of
 RT schizophrenia.";
 RL Biochem. Biophys. Res. Commun. 209:513-518 (1995).
 [8]
 RP VARIANT GLU-76.
 RP MEDLINE=96253892; PubMed=8925252;
 RA Arinami T., Takekoshi K., Itokawa M., Hamaguchi H., Toru M.,
 RA "Failure to find associations of the CA repeat polymorphism in the
 RT first intron and the Gln-63/Glu-63 polymorphism of the neurotrophin-3
 RL gene with schizophrenia.";
 RL Psychiatr. Genet. 6:13-15 (1996).
 [9]
 RP FUNCTION: SEEMS TO PROMOTE THE SURVIVAL OF VISCERAL AND
 RP PROPRIOCEPTIVE SENSORY NEURONS.
 [10]
 RP SUBCELLULAR LOCATION: Secreted.
 [11]
 RP TISSUE SPECIFICITY: BRAIN AND PERIPHERAL TISSUES.
 [12]
 RP POLYMORPHISM: Variant Glu-76 (frequently reported as Glu-63) was
 CC thought to be associated with severe forms of schizophrenia. This
 CC does not seem to be the case.
 [13]
 RP SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
 [14]
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 DR EMBL; X53655; CA937703.1; -
 DR EMBL; M37763; AAA59953.1; -
 DR EMBL; M61180; AAA63231.1; -
 DR PIR; JH0141; JH0141.
 DR PIR; A36208; A36208.
 DR PIR; S10719; S10719.
 DR PIR; C40304; C40304.
 DR PDB; 1BND; 04-APR-96.
 DR PDB; 1B8K; 09-FEB-99.
 DR Genew; HGNC:8023; NTF3.
 DR MIM; 162650; -
 DR InterPro; IPR002400; GF_cysknct.
 DR InterPro; IPR002072; NGF.
 DR Pfam; PF00243; NGF_1.
 DR PRINTS; PR00438; GFCYSKNCT.
 DR PRINTS; PR00268; NGF.
 DR Prodom; PD002052; NGF_1.
 DR SMART; SM00140; NGF_1.
 DR PROSITE; PS00248; NGF_1; 1.
 DR PROSITE; PS02070; NGF_2; 1.
 KW Growth factor; Signal; Polymorphism; 3D-structure.
 FT SIGNAL 1 16
 FT PROPEP 17 128
 FT CHAIN 139 257
 FT DISULFID 152 217
 FT DISULFID 195 246
 FT DISULFID 205 248
 FT CARBOHYD 131 131
 FT VARIANT 76 76
 FT
 FT N-LINKED (GLUCNAC. . .) (POTENTIAL).
 FT G->E.
 FT /FTID=VAR_012084.
 SQ SEQUENCE 257 AA; 29354 MW; 39A5BB3B28E25E03 CRC64;
 Query Match 37.9%; Score 481.5; DB 1; Length 257;
 Best Local Similarity 40.7%; Pred. No. 2e-38; Mismatches 88; Indels 31; Gaps 6;
 Matches 107; Conservative 37; Mismatches 88; Indels 31; Gaps 6;
 QY 1 MSMLFYTLITFLIGIQAPHSSENVPAHGTIPQV-----HWTKLQSLD 45
 DB 1 MSILFYVFLAVLRGIQNMMDQRLPEDSLNLIKIQADILKNTSKMNVKENVQ 60
 QY 46 TALRRA-----RSAPAAIAARVAGQTNITWDPRLF-KRRIRSRVLFSTQPPREA 97
 DB 61 STLPVAPRPRERGPAXSAFOPV-----IAMDTELRQQRVNSPRVILSDTPLEP 114
 QY 98 ADTODLPEVGGAAPFNRTHSKSSSHPIFRGPFVCSVSWVGDKTTATDIKREV 157
 DB 115 PLYIMEDYVSPVYVANTSRKRYAEK-SHREGYVCSDESIMVTDKSSAIDIRHQV 173
 QY 158 MYLGEVININSVFQYFEETKCRDPNPVDSGCRGIDSGKMSYCTTTTFKALTMQ-GK 216
 DB 174 TVLGEIKTNGSPVQYFEETKCRARPVKNGCRGIDSGKMSYCTTTTFKALTMQ 233
 QY 217 QANRFRITIDPACTVLSRRAVR 239
 DB 234 LVGWRWIRIDPISCVCAISRKIGR 256
 RESULT 14
 ID NT3_XENLA STANDARD; PRT; 260 AA.
 AC P25435;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Neurotrophin-3 precursor (NT-3) (Neurotrophic factor) (HDNF) (Nerve
 OS Xenopus laevis (African clawed frog).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
 CC Xenopodinae; Xenopus.

OX NCBI_TaxID=8355;
 RN [1] -
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=97252639; PubMed=9096131;
 RA Xie K., Wang T., Olafsson P., Mizuno K., Lu B.;
 RT Activity-dependent expression of NT-3 in muscle cells in culture:
 RL implications in the development of neuromuscular junctions.";
 RN J. Neurosci. 17:2947-2958(1997).
 RN [2]
 RP SEQUENCE OF 197-217 FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=91222573; PubMed=2025430;
 RA Halboeck F., Ibanez C.F., Persson R.;
 RT Evolutionary studies of the nerve growth factor family reveal a
 RL novel member abundantly expressed in Xenopus ovary.";
 RN Neuron 6:845-858(1991).
 CC -1- FUNCTION: SEEMS TO PROMOTES THE SURVIVAL OF VISCERAL AND
 CC PROPRIOCEPTIVE SENSORY NEURONS.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
 CC -----
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 CC -----
 CC EMBL, U27576; AAB17723.1; -
 CC HSSP; P20783; 188K.
 CC InterPro; IPR002400; GF_cyknoc.
 CC InterPro; IPR002672; NGF.
 CC Pfam; PF00243; NGF; 1.
 CC PRINTS; PR00438; GFCYSKNOT.
 CC PRINTS; PR00268; NGF.
 CC ProDom; PD002052; NGF; 1.
 CC SMART; SM00140; NGF; 1.
 CC PROSITE; PS00248; NGF_1; 1.
 CC PROSITE; PS50270; NGF_2; 1.
 CC Growth factor; Signal.
 CC SIGNAL 1 16 POTENTIAL.
 CC PROPEP 17 141
 CC CHAIN 142 260 NEUROTROPHIN-3.
 CC DISULFID 155 220 BY SIMILARITY.
 CC DISULFID 198 249 BY SIMILARITY.
 CC DISULFID 208 251 BY SIMILARITY.
 CC CARBOHYD 134 134 N-LINKED (GLCNAC...) (POTENTIAL).
 CC SEQUENCE 260 AA; 30022 MW; FFB8507A5E8A33C65 CRC64;
 SO
 Query Match 37.3%; Score 474; DB 1; Length 260;
 Best Local Similarity 41.5%; Pred. No. 1e-37;
 Matches 108; Conservative 36; Mismatches 94; Indels 22; Gaps 7;
 Oy 1 MSMLFTLTITLTAFLIGIAEPHSESNVPAQH-----ITPQVHMTK---LQHSIDTALARRA 51
 Db 1 MSILFTVWFPLPYLGGIHATNNDKKNLPENSNLSPIKLIQADILKKNISKQTVDTKKNHQ 60
 Oy 52 RSAPAAIAARVAGQTRN-----ITVDPLTF---KKRLRSPRVLFSTQPPREADTQ 101
 Db 61 STIRKQILLDDDDNNKKDQFQVVISLALVQCKQRKRSRVLISDSLPLEPPPLY 120
 Oy 102 DLDEVGGAAPF-NRTIRSKRSSHPITFRGSEFVCDSSVWVGDKTTATDICKKEVMVL 160
 Db 121 LMDYIIGHSTVNNRSTRKRKFAEHK-GHRGEYSVCDSSESLMTDKNALDIRHQYTLV 179
 Oy 161 GEVAINNSVFKQYFETKCRDPNVDSCGIGIDSKHNSVYTTHTYVAKLMD-GKQAA 219
 Db 180 GEITGNSPVKQYFETKCRDPNVDSCGIGIDSKHNSVYTTHTYVAKLMD-GKQAA 219
 Oy 220 WRIRIDTACVCLSRKAVR 239
 ||:||||:|||||

DB 240 WRIRIDTACVCLSRKIGR 259
 RESULT 15
 ID NT3_FELCA STANDARD; PRT; 257 AA.
 AC 09ST12;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Neurotrophin-3 precursor (NT-3) (Neurotrophic factor) (HDNF)
 DE (Nerve growth factor 2) (NGF-2).
 GN NT3.
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Placentalia; Feliidae; Felis.
 OC NCBI_TaxID=9685;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20211727; PubMed=10745216;
 RA Lein E.S., Hohn A., Shatz C.J.;
 RT "Dynamic regulation of BDNF and NT-3 expression during visual system
 RL development";
 RL J. Comp. Neurol. 420:1-18(2000).
 CC -1- FUNCTION: SEEMS TO PROMOTES THE SURVIVAL OF VISCERAL AND
 CC PROPRIOCEPTIVE SENSORY NEURONS (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
 CC -----
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 CC -----
 CC EMBL; AF192538; AAF03424.1; -
 CC HSSP; P20783; 188K.
 CC InterPro; IPR002072; NGF.
 CC Pfam; PF00243; NGF; 1.
 CC PRINTS; PR00268; NGF.
 CC ProDom; PD002052; NGF; 1.
 CC SMART; SM00140; NGF; 1.
 CC PROSITE; PS00248; NGF_1; 1.
 CC PROSITE; PS50270; NGF_2; 1.
 CC Growth factor; Signal.
 CC SIGNAL 1 16 POTENTIAL.
 CC PROPEP 17 138
 CC CHAIN 139 257 NEUROTROPHIN-3.
 CC DISULFID 152 217 BY SIMILARITY.
 CC DISULFID 195 246 BY SIMILARITY.
 CC DISULFID 205 248 BY SIMILARITY.
 CC CARBOHYD 131 131 N-LINKED (GLCNAC...) (POTENTIAL).
 CC SEQUENCE 257 AA; 29403 MW; EB53F7B59C511B4 CRC64;
 SO
 Query Match 37.3%; Score 473.5; DB 1; Length 257;
 Best Local Similarity 40.1%; Pred. No. 1e-37;
 Matches 103; Conservative 40; Mismatches 95; Indels 19; Gaps 5;
 Oy 1 MSMLFTLTITLTAFLIGIAEPHSESNVPAQTIPQV-----HMTKLQHSID 45
 Db 1 MSILFTVIFLAYLRGIGNNMDQSRSLPEDLSNLSIKLIQADILKKNLSKQVDTKKNHQ 60
 Oy 46 TARRARSAAPAAIAARVAGQTRNIT-VPRLFK-KKRLRSPRVLFSTQPPREADTQD 103
 Db 61 STIPKADAPREPOGAPASBFQVPMDELRRQRRSSPVLISDSTPLEPPPLYLM 120
 Oy 104 DFEVGAAPFNRTIRSKRSSHPITFRGSEFVCDSSVWVGDKTTATDICKKEVMVL 163
 Db 121 EDVVGSPVAAANRSTRKRKFAEHK-SHRGEYSICDSSESLMTDKNSAIDIRHQYTLVGEI 179
 Oy 164 NINNSVFKQYFETKCRDPNVDSCGIGIDSKHNSVYTTHTYVAKLMD-GKQAAWRP 222
 ||:||||:|||||

Db 180 KSGNSPVKQYFETRCCKEAPVKNCGCGIDDKHMNSQCTTSQTYVRALTSNNKLVGMW 239

Qy 223 IRIDTACVCLSRKAVR 239

Db 240 IRIDTSCVCLSRKIGR 256

Search completed: June 6, 2003, 10:49:54
Job time : 10 secs

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OM protein - protein search, using sw model

Run on: June 6, 2003, 10:47:52 ; Search time 15 Seconds
(without alignments)
1544.560 Million cell updates/sec

Title: US-09-788-188-1

Perfect score: 1270

Sequence: 1 MSMLFYTLITAFILGIGQAEPP.....FIRIDTACVCVSRRAVRA 241

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 73: *
1: p1r1: *
2: p1r2: *
3: p1r3: *
4: p1r4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1270	100.0	286	1 NCHUDM	nerve growth facto
2	1124	88.5	229	2 146614	nerve growth facto
3	1107	87.2	245	2 156570	nerve growth facto
4	1096	86.3	307	1 NGMSWG	beta-nerve growth
5	1092	86.0	241	2 JI0097	nerve growth facto
6	1073	84.5	303	1 NGRTRA	nerve growth facto
7	788.5	62.1	243	2 A26311	nerve growth facto
8	773	60.9	235	2 S14481	nerve growth facto
9	675.5	53.2	243	2 151193	nerve growth facto
10	658	51.8	155	2 A26312	nerve growth facto
11	649	51.1	246	2 A59218	nerve growth facto
12	484	38.1	117	2 S28151	nerve growth facto
13	481.5	37.9	124	2 151709	nerve growth facto
14	481.5	37.9	257	2 C40304	nerve growth facto
15	472	37.2	258	2 S09155	nerve growth facto
16	471.5	37.1	257	2 150400	nerve growth facto
17	471	37.1	282	2 A35781	nerve growth facto
18	452.5	35.6	116	1 NGNMXI	nerve growth facto
19	448.5	35.3	116	1 A58566	nerve growth facto
20	436	33.5	286	2 S50855	nerve growth facto
21	365	28.7	247	2 A40304	nerve growth facto
22	364	28.7	249	2 B40304	nerve growth facto
23	360	28.3	249	2 S12555	nerve growth facto
24	358.5	28.2	252	2 A30361	nerve growth facto
25	348.5	27.0	248	2 JC6183	nerve growth facto
26	343	26.6	226	2 JH0400	nerve growth facto
27	337.5	26.6	210	2 A42687	nerve growth facto
28	335	26.4	269	2 151708	nerve growth facto
29	330.5	26.0	209	2 B42687	nerve growth facto

30	323.5	25.5	114	2	184765	brain-derived neur
31	316.5	24.9	114	2	150606	brain-derived neur
32	307.5	24.2	114	2	151599	brain-derived neur
33	84.5	6.7	5126	2	840450	ryanodine receptor
34	83	6.5	397	2	S53783	aspartate protease
35	80	6.3	835	2	C97322	probable alpha-ara
36	79.5	6.3	749	2	E86774	hypothetical prote
37	79	6.2	807	2	A53225	ecdysone-induced p
38	78.5	6.2	1095	2	T24061	hypothetical prote
39	78.5	6.2	513	2	A12555	hypothetical prote
40	78.5	6.2	701	2	T52384	hypothetical prote
41	78.5	6.2	742	2	T43520	condensin complex
42	78.5	6.2	1076	2	D82083	cardamomyl-phosphat
43	78.5	6.2	1084	2	B64088	hemoglobin-binding
44	78.5	6.2	1609	2	E87243	probable cation tr
45	78	6.1	323	2	S69647	hypothetical prote

ALIGNMENTS

RESULT 1

NCHUDM
nerve growth factor beta chain precursor - human (fragment)

C/Species: Homo sapiens (man)
C/Date: 19-Feb-1984 #sequence_revision 19-Feb-1984 #text_change 18-Jun-1999

C/Accession: A01399; S10253
R/Ullrich, A.; Gray, A.; Berman, C.; Dull, T.J.

Nature 303, 821-825, 1983
A/Title: Human beta-nerve growth factor gene sequence highly homologous to that of mouse

A/Reference number: A93305; MUID:83244969; PMID:6688123
A/Accession: A01399

A/Molecule type: DNA

A/Residues: 1-286 <URL>

R/Borsani, G.; Pizzuti, A.; Rugazli, E.I.; Pallini, A.; Silani, V.; Sidoli, A.; Scarlato
Nucleic Acids Res. 18, 4020, 1990

A/Title: cDNA sequence of human beta-NGF.
A/Reference number: S10253; MUID:90326556; PMID:2374737

A/Accession: S10253
A/Status: translation not shown

A/Molecule type: mRNA

A/Residues: 46-286 <BOR>

A/Cross-references: EMBL:X52599; NID:929476; PIDN:CA36832.1; PID:Q29477
C/Comment: Nerve growth factor is found in submaxillary gland in large quantities and in

nic sensory ganglia in vivo and in vitro and to increase cellular neurotubule levels ma
C/Genetics:

A/Gene: GDB:NGFB
A/Cross-references: GDB:120233; OMIM:162030

A/Map position: 1p13.1-1p13.1
A/Intons: 41/3

C/Complex: nerve growth factor is composed of two alpha chains, two beta chains, and two
C/Keywords: glycoprotein; growth factor; submandibular gland

F/1-166/Domain: signal sequence and propeptide (fragment) #status predicted <SIG>
F/167-284/Product: nerve growth factor beta chain #status predicted <MAT>

F/26,114,159,211/Binding site: carbohydrate (asn) (covalent) #status predicted
F/181-246,224-274,224-276/disulfide bonds: #status predicted

Query Match 100.0%; Score 1270; DB 1; Length 286;
Best Local Similarity 100.0%; Pred. No. 6, 2e-112;
Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MSMLFYTLITAFILGIGQAEPPHSHSNYPAGHTTPOVWMTLQHSIDTALRRARAPAAIA 60
DB	46	MSMLFYTLITAFILGIGQAEPPHSHSNYPAGHTTPOVWMTLQHSIDTALRRARAPAAIA 105
QY	61	ARVAGQTRNITVDPRFLFKRRRLSPVLFSTOPPREAADTODLDFVGAAPNRTTRSK 120
DB	106	ARVAGQTRNITVDPRFLFKRRRLSPVLFSTOPPREAADTODLDFVGAAPNRTTRSK 165
QY	121	RSSSHPIFRGERSVCDSDVWVGDKTTATDIKGKEMVLGEVINNSVFKOYFFETKR 180
DB	166	RSSSHPIFRGERSVCDSDVWVGDKTTATDIKGKEMVLGEVINNSVFKOYFFETKR 225

QY 181 DPNVDSGCRGIDSKHNSVCTTHTFVKALTMGKQAMRFIRIDTACVLSRKAVR 240
 DB 226 DPNVDSGCRGIDSKHNSVCTTHTFVKALTMGKQAMRFIRIDTACVLSRKAVR 285
 QY 241 A 241
 DB 286 A 286

RESULT 2

146614
 nerve growth factor B - pig (fragment)
 C/Species: Sus scrofa domestica (domestic pig)
 C/Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 16-Jul-1999
 C/Accession: 146614
 R/LabIdb-Mansais, Y., Mellink, C., Yerde, M., Gellin, J.
 Cytogenet. Cell Genet. 67, 120-125, 1994
 A/Title: A new marker (NGFB) on pig chromosome 4, isolated by using consensus sequence
 A/Reference number: 146614; MUID:94313891; PMID:8039422
 A/Accession: 146614
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-229 <LAH>
 A/Cross-references: GB:IJ3898; NID:9476732; PIDN:AAA21301.1; PID:9533771
 C/Genetics:
 A/Gene: NGFB
 C/Superfamily: nerve growth factor beta chain

Query Match 88.54; Score 1124; DB 2; Length 229;
 Best Local Similarity 92.64; Pred. No. 2.7e-99;
 Matches 212; Conservative 4; Mismatches 13; Indels 0; Gaps 0;

QY 13 LIGIOAPPHSNNVPAHTIPVHMTLQHSIDTALRRASAPAAIAAVACOTNITV 72
 DB 1 LIGIOAPPHSNNVPAHTIPVHMTLQHSIDTALRRASAPAAIAAVACOTNITV 60
 QY 73 DPLFLFKRRRLRSRVLFTSTPPREADTODLDFEVGAAPFNTTHRSKSSHPFTHRG 132
 DB 61 DPLFLFKRRRLRSRVLFTSTPPREADTODLDFEVGAAPFNTTHRSKSSHPFTHRG 120
 QY 133 FSYCDSSVWVGDKTATIDIKGKVMVLGEVINNSVFKQYFETTCRDPNPVDSGCRGI 192
 DB 121 FSYCDSSVWVGDKTATIDIKGKVMVLGEVINNSVFKQYFETTCRDPNPVDSGCRGI 180
 QY 193 DSGHNSVCTTHTFVKALTMGKQAMRFIRIDTACVLSRKAVR 241
 DB 181 DSGHNSVCTTHTFVKALTMGKQAMRFIRIDTACVLSRKAVR 229

RESULT 3

156570
 beta-nerve growth factor - rat (fragment)
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 16-Jul-1999
 C/Accession: 156570
 R/Whitehead, S.R., Friedman, P.L., Larhammar, D.G., Peterson, H., Gonzalez-Carvajal, M.,
 J. Neurosci. Res. 20, 403-410, 1988
 A/Title: Rat beta-nerve growth factor sequence and site of synthesis in the adult hippoc
 A/Reference number: 156570; MUID:89037223; PMID:3184206
 A/Accession: 156570
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-245 <RES>
 A/Cross-references: GB:M36589; NID:9205691; PIDN:AAA1697.1; PID:9205692
 C/Superfamily: nerve growth factor beta chain

Query Match 87.24; Score 1107; DB 2; Length 245;
 Best Local Similarity 85.84; Pred. No. 1.2e-96;
 Matches 206; Conservative 14; Mismatches 20; Indels 0; Gaps 0;

QY 1 MSMLFTLTITAFILIGIOAPPHSNNVPAHTIPVHMTLQHSIDTALRRASAPAAIA 60
 DB 1 MSMLFTLTITAFILIGIOAPPHSNNVPAHTIPVHMTLQHSIDTALRRASAPAAIA 60

DB 5 MSMLFTLTITAFILIGIOAPPHSNNVPAHTIPVHMTLQHSIDTALRRASAPAAIA 64
 QY 61 ARVAGOTRNTITVDPRLFKRRRLRSRVLFTSTPPREADTODLDFEVGAAPFNTTHRSK 120
 DB 65 ARVAGOTRNTITVDPRLFKRRRLRSRVLFTSTPPREADTODLDFEVGAAPFNTTHRSK 124
 QY 121 RSSHPIFRGESSVCDSSVWVGDKTATIDIKGKVMVLGEVINNSVFKQYFETTCR 180
 DB 125 RSSHPIFRGESSVCDSSVWVGDKTATIDIKGKVMVLGEVINNSVFKQYFETTCR 184
 QY 181 DPNVDSGCRGIDSKHNSVCTTHTFVKALTMGKQAMRFIRIDTACVLSRKAVR 240
 DB 185 DPNVDSGCRGIDSKHNSVCTTHTFVKALTMGKQAMRFIRIDTACVLSRKAVR 244

RESULT 4

NGMSMG
 nerve growth factor beta chain precursor - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 30-Nov-1980 #sequence_revision 19-Feb-1984 #text_change 21-Jul-2000
 C/Accession: A93301; A93305; A90366; 149689; 152891; A01400; 149690
 R/Scott, J., Selby, M., Urdeda, M., Quiroga, M., Bell, G.T., Rutter, W.J.
 Nature 302, 538-540, 1983
 A/Title: Isolation and nucleotide sequence of a cDNA encoding the precursor of mouse r
 A/Reference number: A93301; MUID:83167518; PMID:6336309
 A/Accession: A93301
 A/Molecule type: mRNA
 A/Residues: 1-307 <SCO>
 A/Cross-references: GB:V00836; NID:953364; PIDN:CAA24221.1; PID:953365
 R/Ollrich, A., Gray, A., Berman, C., Dull, T.J.
 Nature 303, 821-825, 1983
 A/Title: Human beta-nerve growth factor gene sequence highly homologous to that of mou
 A/Reference number: A93305; MUID:83244969; PMID:6688123
 A/Accession: A93305
 A/Molecule type: mRNA
 A/Residues: 1-307 <ULB>
 A/Cross-references: GB:K01759; NID:9200051; PIDN:AAA39820.1; PID:9387495
 A/Note: these authors believe that Met-67 is probably the amino-terminal residue and t
 R/Angelini, R.H., Herndon, M.A., Bradshaw, R.A.
 Biochemistry 12, 100-115, 1973
 A/Title: Amino acid sequences of mouse 2.5S nerve growth factor. II. Isolation and cha
 A/Reference number: A90366; MUID:73075048; PMID:4566923
 A/Accession: A90366
 A/Molecule type: protein
 A/Residues: 188-216; N/218-305 <ANG>
 R/Selby, M.J., Edwards, R., Sharp, P., Rutter, W.J.
 Mol. Cell. Biol. 7, 3057-3064, 1987
 A/Title: Mouse nerve growth factor gene: Structure and expression.
 A/Reference number: 149689; MUID:88038855; PMID:3670305
 A/Accession: 149689
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-307 <RES>
 A/Cross-references: GB:M17298; NID:9193493; PIDN:AAA37687.1; PID:9467311
 R/Ollrich, A., Gray, A., Berman, C.H., Coussens, L., Dull, T.J.
 Cold Spring Harb. Symp. Quant. Biol. 48, 435-442, 1983
 A/Title: Sequence homology of human and mouse beta-NGF subunit genes.
 A/Reference number: 152891; MUID:84206565; PMID:6327169
 A/Accession: 152891
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-307 <RES>
 A/Cross-references: GB:M14805; NID:9200053; PIDN:AAA39821.1; PID:9200054
 C/Comment: The active molecule is a dimer of identical chains associated by noncovalen
 nic sensory ganglia in vivo and in vitro and to increase cellular neurotubule levels m
 C/Genetics:
 A/Gene: NGFB
 A/Introns: 21/21 62/3
 C/Superfamily: nerve growth factor beta chain
 C/Keywords: glycoprotein; growth factor; homodimer
 F.1-187/Domain: signal sequence and propeptide #status predicted <Sig>
 F.188-305/Product: nerve growth factor beta chain #status experimental <Mat>

F135,180/Binding site: carbohydrate (asn) (covalent) #status predicted
F1202,267,245-295,255-297/Diulfide bonds: #status experimental
F1232/Binding site: carbohydrate (asn) (covalent) #status absent

Query Match 86.3%; Score 1096; DB 1; Length 307;
Best Local Similarity 85.0%; Pred. No. 1,76-95;
Matches 204; Conservative 14; Mismatches 22; Indels 0; Gaps 0;

QY 1 MSMLFYTLITAFILGIAEPHSESNVPAGHTIPQVHTKLOHSLDTALRRASAPAAIA 60
DB 67 MSMLFYTLITAFILGIAEPHSESNVPAGHTIPQVHTKLOHSLDTALRRASAPAAIA 126
QY 61 ARVAGQTRNITVDPRLFKKRLRSPRYLFTSTQPREADTODLDFEVGAAPFNRTTRSK 120
DB 127 ARVAGQTRNITVDPRLFKKRLRSPRYLFTSTQPREADTODLDFEVGAAPFNRTTRSK 186
QY 121 RSSHPHFHGESEVCSVSWVGDKTTADIKKEVMTLGEVINNSVFKQYFEETKCR 180
DB 187 RSSHPHFHGESEVCSVSWVGDKTTADIKKEVMTLGEVINNSVFKQYFEETKCR 246
QY 181 DPNPVDSCRGIDSKHNSYCTTHTTFVKALITMDGKOAMRIRIDTACVLSKRAVR 240
DB 247 ASNPVSGCRGIDSKHNSYCTTHTTFVKALITMDGKOAMRIRIDTACVLSKRAVR 306

RESULT 5

JL0097
nerve growth factor beta chain precursor - guinea pig

C/Species: Cavia porcellus (guinea pig)
C/Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 15-Mar-1996
C/Accession: JL0097

R/Schwartz, M.A.; Fisher, D.; Bradshaw, R.A.; Isaacson, P.J.
J. Neurochem. 52, 1203-1209, 1989

A/Title: Isolation and sequence of a cDNA clone of beta-nerve growth factor from the guinea pig
A/Reference number: JL0097; MUID:89177243; PMID:2926397
A/Accession: JL0097
A/Molecule type: mRNA
A/Residues: 1-241 <SC>
A/Note: the authors translated the codon GCU for residue 214 as Asp

C/Genetics:
A/Gene: Beta-NGF
C/Superfamily: nerve growth factor beta chain
C/Keywords: glycoprotein; growth factor; hormone
F1-121/Domain: propeptide #status predicted <PRO>
F122-241/Product: nerve growth factor beta chain #status predicted <MAT>
F146-154/Region: receptor binding #status predicted
F169,114/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 86.0%; Score 1092; DB 2; Length 241;
Best Local Similarity 86.2%; Pred. No. 2,96-95;
Matches 207; Conservative 10; Mismatches 23; Indels 0; Gaps 0;

QY 1 MSMLFYTLITAFILGIAEPHSESNVPAGHTIPQVHTKLOHSLDTALRRASAPAAIA 60
DB 1 MSMLFYTLITAFILGIAEPHSESNVPAGHTIPQVHTKLOHSLDTALRRASAPAAIA 60
QY 61 ARVAGQTRNITVDPRLFKKRLRSPRYLFTSTQPREADTODLDFEVGAAPFNRTTRSK 120
DB 61 ARVAGQTRNITVDPRLFKKRLRSPRYLFTSTQPREADTODLDFEVGAAPFNRTTRSK 120
QY 121 RSSHPHFHGESEVCSVSWVGDKTTADIKKEVMTLGEVINNSVFKQYFEETKCR 180
DB 121 RSSHPHFHGESEVCSVSWVGDKTTADIKKEVMTLGEVINNSVFKQYFEETKCR 180
QY 181 DPNPVDSCRGIDSKHNSYCTTHTTFVKALITMDGKOAMRIRIDTACVLSKRAVR 240
DB 181 DPNPVDSCRGIDSKHNSYCTTHTTFVKALITMDGKOAMRIRIDTACVLSKRAVR 240

RESULT 6

NGRTBA
nerve growth factor beta chain precursor - multimammate rat (Mastomys natalensis)
C/Species: Mastomys natalensis

C/Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 18-Jun-1999
C/Accession: J03343
R/Fahnestock, M.; Bell, R.A.
Gene 69, 257-264, 1988

A/Title: Molecular cloning of a cDNA encoding the nerve growth factor precursor from Mastomys natalensis
A/Reference number: J03343; MUID:89172070; PMID:3234767
A/Accession: J03343
A/Molecule type: mRNA
A/Residues: 1-303 <FAH>

A/Cross-references: GB:M22748; NID:G202514; PID:AAA40599.1; PID:G202515
A/Note: It is uncertain whether Met-1 or Met-63 is the initiator
C/Superfamily: nerve growth factor beta chain
C/Keywords: glycoprotein; growth factor; homodimer; submaxillary gland

F184-301/Product: nerve growth factor beta chain #status predicted <MAT>
F131,176,228/Binding site: carbohydrate (asn) (covalent) #status predicted
F198-263,241-291,251-293/Diulfide bonds: #status predicted

Query Match 84.5%; Score 1073; DB 1; Length 303;
Best Local Similarity 83.3%; Pred. No. 2,46-93;
Matches 200; Conservative 17; Mismatches 23; Indels 0; Gaps 0;

QY 1 MSMLFYTLITAFILGIAEPHSESNVPAGHTIPQVHTKLOHSLDTALRRASAPAAIA 60
DB 63 MSMLFYTLITAFILGIAEPHSESNVPAGHTIPQVHTKLOHSLDTALRRASAPAAIA 122
QY 61 ARVAGQTRNITVDPRLFKKRLRSPRYLFTSTQPREADTODLDFEVGAAPFNRTTRSK 120
DB 123 ARVAGQTRNITVDPRLFKKRLRSPRYLFTSTQPREADTODLDFEVGAAPFNRTTRSK 182
QY 121 RSSHPHFHGESEVCSVSWVGDKTTADIKKEVMTLGEVINNSVFKQYFEETKCR 180
DB 183 RSSHPHFHGESEVCSVSWVGDKTTADIKKEVMTLGEVINNSVFKQYFEETKCR 242
QY 181 DPNPVDSCRGIDSKHNSYCTTHTTFVKALITMDGKOAMRIRIDTACVLSKRAVR 240
DB 243 ARNPVSGCRGIDSKHNSYCTTHTTFVKALITMDGKOAMRIRIDTACVLSKRAVR 302

RESULT 7

A26311
nerve growth factor beta chain precursor - chicken (fragment)

C/Species: Gallus gallus (chicken)
C/Date: 05-Oct-1988 #sequence_revision 05-Oct-1988 #text_change 21-Jul-2000
C/Accession: A26311; A24857; S00127; S12532
R/Ebendal, T.; Larhammar, D.; Persson, H.
EMBO J. 5, 1483-1487, 1986

A/Title: Structure and expression of the chicken beta nerve growth factor gene.
A/Reference number: A26311; MUID:86300646; PMID:3017695
A/Accession: A26311
A/Molecule type: mRNA
A/Residues: 1-243 <EBE>

A/Cross-references: GB:X04003; NID:G63697; PID:CAA27633.1; PID:g1334740
R/Mon, D.; Perret, C.; Frech, N.; Keller, A.; Behar, G.; Brachet, P.; Aufferay, C.
FEBS Lett. 203, 82-86, 1986
A/Title: Molecular cloning of the avian beta-nerve growth factor gene: transcription in

A/Reference number: A24857; MUID:86248129; PMID:3720959
A/Accession: A24857
A/Molecule type: DNA
A/Residues: 118-243 <MIO>

A/Cross-references: GB:D00010; GB:N00010; GB:X04067; NID:G222840; PID:BA00008.1; PID:R1000000.1; PID:R1000000.1; PID:R1000000.1
R/Mon, D.; Perret, C.; Frech, N.; Keller, A.; Behar, G.; Brachet, P.; Aufferay, C.
EMBO J. 5, 1489-1493, 1986
A/Title: Molecular cloning of the avian beta-nerve growth factor gene: transcription in

A/Reference number: A26312; MUID:86300647; PMID:2427334
A/Accession: S00127
A/Molecule type: DNA
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: DNA
A/Residues: 121-243 <MEI>

A/Cross-references: GB:M26810; NID:G212446; PID:AAA48964.1; PID:G212447
R/Ibanez, C.F.; Halibosek, F.; Ebendal, T.; Persson, H.
EMBO J. 9, 1477-1483, 1990
A/Title: Structure-function studies of nerve growth factor: functional importance of his
A/Reference number: S12532; MUID:90228346; PMID:2328722

A/Accession: S12532
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 126-243 <1BA>
 C/Superfamily: nerve growth factor beta chain
 C/Keywords: growth factor
 F/1-125/Domain: signal sequence #status predicted <SIG>
 F/126-243/Product: nerve growth factor beta chain #status predicted <MAT>

Query Match 62.1%; Score 788.5; DB 2; Length 243;
 Best Local Similarity 64.9%; Pred. No. 1,1e-66;
 Matches 161; Conservative 20; Mismatches 48; Indels 19; Gaps 6;

QY 1 MSMLFTYLLTAFLIGIOAEPHSSSNVPAHT---IP-QVHWTK-LQHSIDTALRRARSA 56
 DB 5 MSMLYTLTLLTAFLIGIOAEPKSDNGPLEPAEHSLSPTQOSNGCHI-----AKAPQ 57
 QY 57 AAIARVA-----GQTRNITVDPLRPFKKRLRSRVLFTSTOPPREADTODLDFEVGAA 111
 DB 58 TT-HGRFAMPDGDIEDLNINADQNFKKKRRSSSLVFTSTOPPPVSRKQSTGF-LSSAV 115
 QY 112 PFNTHRSKRSSSHPIFRGSEFVSVDVSVWVGDKTTATDIDKKEVWVLGEVNNINSVFK 171
 DB 116 SLNRTATKTR-TAHPVLRGSEFVSVDVSVWVGDKTTATDIDKKEVWVLGEVNNINSVFK 174
 QY 172 QYFETKCRDPNPVDSGCRGIDSKHNSYCTTHTFYKALTMGKQAAAFRIRIDTACVC 231
 DB 175 QYFETKCRDPNPVDSGCRGIDAKHNSYCTTHTFYKALTMGKQAAAFRIRIDTACVC 234
 QY 232 VLSRKAVR 239
 DB 235 VLSRKSGR 242

RESULT 8

S14481
 nerve growth factor beta chain precursor - African clawed frog
 C/Species: Xenopus laevis (African clawed frog)
 C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 16-Jul-1999
 C/Accession: S14481
 R/Carrier: F.; Campbell, M.; Cardinali, B.; Pierandrei-Amaldi, P.
 A/Submitted to the EMBL Data Library: October 1990
 A/Description: Structure and expression of the nerve growth gene in Xenopus oocyte and e
 A/Reference number: S14481
 A/Accession: S14481
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-235 <CAR>
 A/Cross-references: EMBL:X55716; NID:g64914; PIRN:CAA39249.1; PID:g64915
 C/Superfamily: nerve growth factor beta chain

Query Match 60.9%; Score 773; DB 2; Length 235;
 Best Local Similarity 63.6%; Pred. No. 3.2e-65;
 Matches 154; Conservative 27; Mismatches 41; Indels 20; Gaps 6;

QY 1 MSMLFTYLLTAFLIGIOAEPHSSSNVPAHT---IP-QVHWTK-LQHSIDTALRRARSA 54
 DB 5 MSMLYTLTLLTAFLISVQAAPKTKDHAARSSAKSRIPHHTHRTKSLHS-----53
 QY 55 PAALAAARVAGQTNITVDPLRPFKKRLRSRVLFTSTOPPREADTODLDFEVGAAPFN 114
 DB 54 -HGKLEAKERSYFRNVTVDPLRPFKKRFRSPRVLFSTOPPLEDFQHLEY-LDDEESLN 111
 QY 115 RTHRSKRSSSHPIFRGSEFVSVDVSVWVGDKTTATDIDKKEVWVLGEVNNINSVFKQYF 174
 DB 112 KTRARAK-TAHPVLRGSEFVSVDVSVWVGDKTTATDIDKKEVWVLGEVNNINSVFKQYF 170
 QY 175 FETKCRDPNPVDSGCRGIDSKHNSYCTTHTFYKALTMGKQAAAFRIRIDTACVC 234
 DB 171 FETKCRDPNPVDSGCRGIDAKHNSYCTTHTFYKALTMGKQAAAFRIRIDTACVC 230
 QY 235 RK 236

DB 231 RK 232

RESULT 9

151193
 nerve growth factor precursor - many-banded krait
 C/Species: Bungarus multicinctus (many-banded krait)
 C/Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Jul-1999
 C/Accession: 151193
 R/Dansey, J.M.; Garnier, J.M.
 A/Title: Molecular cloning of a cDNA encoding a nerve growth factor precursor from th
 A/Reference number: 151193; MUID:93192074; PMID:7916740
 A/Accession: 151193
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-243 <DAN>
 A/Cross-references: GB:S56212; NID:g266298; PIRN:AA825729.1; PID:g266299
 C/Superfamily: nerve growth factor beta chain

Query Match 53.2%; Score 675.5; DB 2; Length 243;
 Best Local Similarity 56.8%; Pred. No. 5e-56;
 Matches 137; Conservative 30; Mismatches 67; Indels 7; Gaps 4;

QY 1 MSMLFTYLLTAFLIGIOAEPHSSSNVPAHT---HTIPQVHWTKLQHSIDTALRRARSA 56
 DB 1 MSMLCYTLTLLTAFLIGIWAAPKSESDNVLGSPAKSDSDTNCAGTHGLKTSRNTDQHPT 60
 QY 57 AAIARVA-----GQTRNITVDPLRPFKKRLRSRVLFTSTOPPREADTODLDFEVGAAPFN 115
 DB 61 PKSEDOELGSAANNITVDPLRPFKKRFRSPRVLFSTOPPLESRDEQVKE-LTDEDTLNR 119
 QY 116 THRSKRSSSHPIFRGSEFVSVDVSVWVGDKTTATDIDKKEVWVLGEVNNINSVFKQYF 175
 DB 120 NINA-NNEHPVANNQSEHSVCDISVWVNTKRIATIDIKGTVVWVDVNNNEVYKQYF 178
 QY 176 ETYCRDPNPVDSGCRGIDSKHNSYCTTHTFYKALTMGKQAAAFRIRIDTACVC 235
 DB 179 ETYCRDPNPVDSGCRGIDSRHNSYCTTHTFYKALTMGKQAAAFRIRIDTACVC 236
 QY 236 K 236
 DB 239 K 239

RESULT 10

A26312
 nerve growth factor beta chain precursor - bovine (fragment)
 C/Species: Bos primigenius taurus (cattle)
 C/Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 16-Jul-1999
 C/Accession: A26312
 R/Meyer, R.; Becker-Andre, M.; Goetz, R.; Heumann, R.; Shaw, A.; Thoenen, H.
 A/Title: Molecular cloning of bovine and chick nerve growth factor (NGF): delineation
 A/Reference number: A26312; MUID:86300647; PMID:2427334
 A/Accession: A26312
 A/Molecule type: mRNA
 A/Residues: 1-125 <MEI>
 A/Cross-references: GB:M26809; NID:g163419; PIRN:AAA3066.1; PID:g163420
 C/Comment: Nerve growth factor stimulates neurite outgrowth from sympathetic and embry
 C/Superfamily: nerve growth factor beta chain
 C/Keywords: growth factor; homodimer; seminal vesicle
 F/6-125/Product: nerve growth factor #status predicted <MAT>
 F/20-85,63-113,73-115/Distal bonds: #status predicted

Query Match 51.8%; Score 658; DB 2; Length 125;
 Best Local Similarity 95.2%; Pred. No. 9.8e-55;
 Matches 119; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 117 HRSKRSSSHPIFRGSEFVSVDVSVWVGDKTTATDIDKKEVWVLGEVNNINSVFKQYF 176
 DB 1 HRSKRSSSHPIFRGSEFVSVDVSVWVGDKTTATDIDKKEVWVLGEVNNINSVFKQYF 60

A, Title: Molecular cloning of a human gene that is a member of the nerve growth factor gene family
A, Reference number: A36208, MUID:91045937, PMID:2236018
A, Accession: A36208

A, Title: Molecular cloning of a human gene that is a member of the nerve growth factor gene family
A, Reference number: A36208, MUID:91045937, PMID:2236018
A, Accession: A36208

A:Molecule type: DNA
 A:Residues: 1-257 <JON>
 A:Cross-references: GB:M37763; NID:g189300; PIDN:AAA5953.1; PID:g189301
 R:Roenthal, A.; Goeddel, D.V.; Nguyen, T.; Lewis, M.; Shih, A.; Laramee, G.R.; Nikolic
 Neuron 4, 767-773, 1990
 A>Title: Primary structure and biological activity of a novel human neurotrophic factor
 A:Reference number: JH0141; MUID:90262727; PMID:2344409
 A:Accession: JH0141
 A:Molecule type: DNA
 A:Residues: 1-257 <ROS>
 R:Malbomplere, P.C.; Le Beau, M.M.; Espinosa III, R.; Ip, N.Y.; Belluscio, L.; de la M
 Genomics 10, 558-568, 1991
 A>Title: Human and rat brain-derived neurotrophic factor and neurotrophin-3: gene struc
 A:Reference number: A40304; MUID:91365361; PMID:1889806
 A:Accession: C40304
 A:Molecule type: DNA
 A:Residues: 1-257 <NAI>
 A:Cross-references: GB:M61180; NID:g189302; PIDN:AAA63231.1; PID:g189303
 R:Kaibho, Y.; Yoshimura, K.; Nakahama, K.
 FEBS Lett. 266, 187-191, 1990
 A>Title: Cloning and expression of a cDNA encoding a novel human neurotrophic factor.
 A:Reference number: S10719; MUID:90306351; PMID:2365067
 A:Accession: S10719
 A:Molecule type: mRNA
 A:Residues: 1-257 <KAI>
 A:Cross-references: GB:X53555; NID:g287794; PIDN:CAA37703.1; PID:g287795
 R:Yancopoulos, G.D.; Malbomplere, P.C.; Ip, N.Y.; Aldrich, T.H.; Belluscio, L.; Boulton
 Cold Spring Harb. Symp. Quant. Biol. 55, 371-379, 1990
 A>Title: Neurotrophic factors, their receptors, and the signal transduction pathways the
 A:Reference number: A60536; MUID:9211157; PMID:1966766
 A:Accession: C60536
 A>Status: not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 1-73, 'Q', 75-77, 'R', 79-108, 'T', 110-257 <YAN>
 A:Gene: GDB:NTP3
 A:Cross-references: GDB:125917; OMIM:162660
 A:Map position: 12p13-12p13
 C:Superfamily: nerve growth factor beta chain
 C:Keywords: glycoprotein
 F:1-18/Domain: signal sequence #status predicted <SIG>
 F:139-257/Domain: propeptide #status predicted <PRO>
 F:139-257/Product: neurotrophin-3 #status predicted <MAT>
 F:131/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 37.9%; Score 481.5; DB 2; Length 257;
 Best Local Similarity 40.7%; Pred. No. 1e-37;
 Matches 107; Conservative 37; Mismatches 88; Indels 31; Gaps 6;

QY 1 MSMLFYTLITAFILGIGQAPHSSENVPAQHTIPQV-----HWTXLQHSID 45
 DB 1 MSILFYVFLAVLRIQGNNDQSLPEDSLNSLIKLIQADILKNKLSKQWVYKENYQ 60
 QY 46 TALARRA-----RSAPAAALAAVAGOTRNTITVDRPLFK-RRRLRSRYLFSTQPPREA 97
 DB 61 STLPRKAEAPREPERGEPKSAFQPV-----IAMDTELRQQRYSNPRVLLSDSTPLRP 114
 QY 98 ADTQDLDFEVGAAPFNRTHSRKSSSHPIFRGSEFVCDSSVWVGDKTTATDIDGKEV 157
 DB 115 PLYLMEDYVGSFVAVANRTSRKRYAEHK-SHGEYSVCDSESLWTDKSSALIDRGHQV 173
 QY 158 MWLGEVNNINSVFKYFFETKCRDNPVDSGCRGIDSKHNSYCTTHTFVKALTMW-GK 216
 DB 174 TVLGEIKTGNSEVVKQYFETRCKEARPVKNGCRGIDDKHNSOCKTSQTYVALTSENK 233
 QY 217 QAAWFRIDTACVCLSRKAVR 239
 DB 234 LVGRWRIRIDTSVCALSRKIGR 256

RESULT 15
 S09155
 neurotrophin-3 precursor - mouse

C:Species: Mus musculus (house mouse)
 C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #ext_change 16-Jul-1999
 C:Accession: S09155; S51179
 R:Rohn, A.; Leebrock, J.; Bailey, K.; Barde, Y.A.
 Nature 344, 339-341, 1990
 A>Title: Identification and characterization of a novel member of the nerve growth fa
 A:Reference number: S09155; MUID:90190865; PMID:2314473
 A:Accession: S09155
 A>Status: not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 1-258 <HOB>
 A:Cross-references: GB:X53257; NID:g53451; PIDN:CAA37348.1; PID:g53452
 R:Kolbeck, R.; Jungbluth, S.; Barde, Y.A.
 Eur. J. Biochem. 225, 995-1003, 1994
 A>Title: Characterisation of neurotrophin dimers and monomers.
 A:Reference number: S51179; MUID:95045576; PMID:7957235
 A:Accession: S51179
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 140-152 <ROL>
 C:Superfamily: nerve growth factor beta chain
 C:Keywords: glycoprotein
 F:1-18/Domain: signal sequence #status predicted <SIG>
 F:140-258/Product: neurotrophin-3 #status predicted <MAT>
 F:131/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 37.2%; Score 472; DB 2; Length 258;
 Best Local Similarity 41.9%; Pred. No. 8e-37;
 Matches 108; Conservative 33; Mismatches 97; Indels 20; Gaps 5;

QY 1 MSMLFYTLITAFILGIGQAPHSSENVPAQHTIPQV-----HWTXLQHSIDTL----- 48
 DB 1 MSILFYVFLAVLRIQGNNDQSLPEDSLNSLIKLIQADILKNKLSKQWVYKENYQ 60
 QY 49 -----RRRKSAPAAALAAVAGOTRNTITVDRPLFKRRLRSRYLFSTQPPREAADTQDL 103
 DB 61 STLPRKAEAPREPERGEPKSAFQPV-----IAMDTELRQQRYSNPRVLLSDSTPLRP 120
 QY 104 DFEVGAAPFNRTH-RSRKSSSHPIFRGSEFVCDSSVWVGDKTTATDIDGKEVMTGE 162
 DB 121 EDYGNFVAVANRTSRKRYAEHK-SHGEYSVCDSESLWTDKSSALIDRGHQVYVIGE 179
 QY 163 VNINSVFKYFFETKCRDNPVDSGCRGIDSKHNSYCTTHTFVKALTMW-GKQAAWR 221
 DB 180 IKTGNSEVVKQYFETRCKEARPVKNGCRGIDDKHNSOCKTSQTYVALTSENKLVGR 239
 QY 222 FIRIDTACVCLSRKAVR 239
 DB 240 WIRIDTSVCALSRKIGR 257

Search completed: June 6, 2003, 10:51:33
 Job time: 17 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 6, 2003, 10:49:38 ; Search time 17.5 Seconds

(without alignments)
1421.766 Million cell updates/sec

Title: US-09-788-188-1

Sequence: 1 MSMFTTITVFLIGIQAEPP.....FIRIDTACVTSRRKAVRRA 241

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 392085 seqs, 103240269 residues

Total number of hits satisfying chosen parameters: 392085

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pdb.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pdb.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pdb.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pdb.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pdb.*
- 6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pdb.*
- 7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pdb.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pdb.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pdb.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pdb.*
- 11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pdb.*
- 12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pdb.*
- 13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pdb.*
- 14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pdb.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1270	100.0	241	8	US-08-450-842-5 Sequence 5, Appl1
2	1270	100.0	241	9	US-09-788-188-1 Sequence 1, Appl1
3	1270	100.0	241	9	US-10-150-262-3 Sequence 1, Appl1
4	1270	100.0	241	9	US-10-155-886-1 Sequence 1, Appl1
5	1270	100.0	241	9	US-10-155-886-6 Sequence 6, Appl1
6	1270	100.0	242	12	US-10-072-681-1 Sequence 1, Appl1
7	1265	99.7	241	10	US-09-822-263-16 Sequence 16, Appl1
8	1265	99.6	241	9	US-09-788-188-2 Sequence 7, Appl1
9	1249	98.3	241	9	US-10-155-886-7 Sequence 7, Appl1
10	1249	98.3	241	9	US-10-155-886-8 Sequence 8, Appl1
11	1106	87.1	231	9	US-10-155-886-10 Sequence 10, Appl1
12	1096	86.3	241	9	US-10-155-886-9 Sequence 9, Appl1
13	788.5	62.1	243	9	US-10-155-886-11 Sequence 11, Appl1
14	773	60.9	235	9	US-10-155-886-12 Sequence 12, Appl1
15	651	51.3	120	9	US-10-150-262-1 Sequence 1, Appl1
16	651	51.3	120	9	US-10-155-886-34 Sequence 34, Appl1
17	648	51.0	121	10	US-10-072-681-2 Sequence 2, Appl1
18	648	51.0	157	12	US-09-798-338-4 Sequence 4, Appl1
19	647.5	51.0	167	10	US-09-798-338-8 Sequence 8, Appl1

20	642	50.6	153	10	US-09-798-338-2 Sequence 2, Appl1
21	642	50.6	163	10	US-09-798-338-6 Sequence 6, Appl1
22	621	48.9	121	9	US-09-813-398-9 Sequence 9, Appl1
23	621	48.7	121	9	US-10-155-886-33 Sequence 33, Appl1
24	602	47.4	120	9	US-10-155-886-36 Sequence 36, Appl1
25	584	46.0	118	9	US-10-155-886-40 Sequence 40, Appl1
26	584	46.0	120	9	US-10-155-886-38 Sequence 38, Appl1
27	584	46.0	121	12	US-10-072-681-3 Sequence 3, Appl1
28	566	44.6	117	9	US-10-155-886-42 Sequence 42, Appl1
29	512	40.3	121	9	US-10-155-886-37 Sequence 37, Appl1
30	505	39.8	125	9	US-10-155-886-35 Sequence 35, Appl1
31	481.5	37.9	257	8	US-08-450-842-4 Sequence 4, Appl1
32	481.5	37.9	257	9	US-09-788-188-5 Sequence 5, Appl1
33	481.5	37.9	257	9	US-10-155-886-3 Sequence 3, Appl1
34	476.5	37.5	257	9	US-09-788-188-6 Sequence 6, Appl1
35	474	37.3	260	9	US-10-155-886-20 Sequence 20, Appl1
36	472	37.2	258	9	US-10-155-886-18 Sequence 18, Appl1
37	471.5	37.1	257	9	US-10-155-886-19 Sequence 19, Appl1
38	471	37.1	258	9	US-10-155-886-17 Sequence 17, Appl1
39	452	35.6	142	8	US-08-450-842-52 Sequence 52, Appl1
40	390	30.7	72	10	US-09-848-664-21 Sequence 21, Appl1
41	388.5	30.6	119	10	US-09-745-032-6 Sequence 6, Appl1
42	388.5	30.6	119	10	US-09-742-600-6 Sequence 6, Appl1
43	388.5	30.6	119	10	US-09-872-090-6 Sequence 3, Appl1
44	388.5	30.6	120	10	US-09-745-032-3 Sequence 3, Appl1
45	388.5	30.6	120	10	US-09-742-600-3 Sequence 3, Appl1

ALIGNMENTS

RESULT 1
US-08-450-842-5
Sequence 5, Application US/08450842
Patent No. US20020045576A1
GENERAL INFORMATION:
APPLICANT: GENE TECH, INC.
APPLICANT: ROSENTHAL, ARNON
TITLE OF INVENTION: NOVEL NEUROTROPHIC FACTOR
NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 Inch, 360 KB floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450, 842
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/426419
FILING DATE: 19-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/030013
FILING DATE: 22-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/648482
FILING DATE: 31-JAN
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/587707
FILING DATE: 1991
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: 666P2C1D3
TELECOMMUNICATION INFORMATION:

TELEPHONE: 415/225-8674
 TELEFAX: 415/952-9881
 TELEEX: 910/371-7168
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 241 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 US-08-450-842-5

Query Match 100.0%; Score 1270; DB 9; Length 241;
 Best Local Similarity 100.0%; Pred. No. 2,3e-124;
 Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MSMLFTLTITAFILGIGQAEPSHESNVPAGHTIPQVHWTKLOHSIDTLRRARSAAPAAIA 60
 1 MSMLFTLTITAFILGIGQAEPSHESNVPAGHTIPQVHWTKLOHSIDTLRRARSAAPAAIA 60
 Qy 61 ARVAGOTRNTITVDPRLFKKRLRSRVLFSSTOPPREAADTODLDFEVGAAPFNRTTRSK 120
 Db 61 ARVAGOTRNTITVDPRLFKKRLRSRVLFSSTOPPREAADTODLDFEVGAAPFNRTTRSK 120
 Qy 121 RSSSHPIFHRGSEFVCDVSVMWGDKTTATDIDKGEVMVLGEVINNSVFQYFFETKCR 180
 Db 121 RSSSHPIFHRGSEFVCDVSVMWGDKTTATDIDKGEVMVLGEVINNSVFQYFFETKCR 180
 Qy 181 DPNPVDGCGRGIDSKMNSYCTTHTFVKALTMDSQAAMRFIRIDTACVLSKAVRR 240
 Db 181 DPNPVDGCGRGIDSKMNSYCTTHTFVKALTMDSQAAMRFIRIDTACVLSKAVRR 240
 Qy 241 A 241
 Db 241 A 241

RESULT 2
 US-09-788-188-1
 Sequence 1, Application US/09788188
 Publication No. US20030040082A1

GENERAL INFORMATION:
 APPLICANT: TUSZYNSKI, MARK
 APPLICANT: BLESCH, ARMIN
 TITLE OF INVENTION: MUTANT PRO-NEUTROPHIN WITH IMPROVED ACTIVITY
 FILE REFERENCE: 041673/2045
 CURRENT APPLICATION NUMBER: US/09/788,188
 CURRENT FILING DATE: 2001-02-16
 NUMBER OF SEQ ID NOS: 16
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 1
 LENGTH: 241
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-788-188-1

Query Match 100.0%; Score 1270; DB 9; Length 241;
 Best Local Similarity 100.0%; Pred. No. 2,3e-124;
 Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MSMLFTLTITAFILGIGQAEPSHESNVPAGHTIPQVHWTKLOHSIDTLRRARSAAPAAIA 60
 1 MSMLFTLTITAFILGIGQAEPSHESNVPAGHTIPQVHWTKLOHSIDTLRRARSAAPAAIA 60
 Qy 61 ARVAGOTRNTITVDPRLFKKRLRSRVLFSSTOPPREAADTODLDFEVGAAPFNRTTRSK 120
 Db 61 ARVAGOTRNTITVDPRLFKKRLRSRVLFSSTOPPREAADTODLDFEVGAAPFNRTTRSK 120
 Qy 121 RSSSHPIFHRGSEFVCDVSVMWGDKTTATDIDKGEVMVLGEVINNSVFQYFFETKCR 180
 Db 121 RSSSHPIFHRGSEFVCDVSVMWGDKTTATDIDKGEVMVLGEVINNSVFQYFFETKCR 180
 Qy 181 DPNPVDGCGRGIDSKMNSYCTTHTFVKALTMDSQAAMRFIRIDTACVLSKAVRR 240
 Db 181 DPNPVDGCGRGIDSKMNSYCTTHTFVKALTMDSQAAMRFIRIDTACVLSKAVRR 240

Qy 241 A 241
 Db 241 A 241

RESULT 3
 US-10-150-262-3
 Sequence 3, Application US/10150262
 Publication No. US20030049264A1
 GENERAL INFORMATION:
 APPLICANT: FOSTER, KEITH ALAN
 APPLICANT: DUGAN, MICHAEL JOHN
 APPLICANT: SHONE, CLIFFORD CHARLES
 TITLE OF INVENTION: CLOSTRIDIAL TOXIN DERIVATIVES ABLE TO MODIFY
 TITLE OF INVENTION: PERIPHERAL
 TITLE OF INVENTION: SENSOR APPARENT FUNCTIONS
 FILE REFERENCE: 023223/0104
 CURRENT APPLICATION NUMBER: US/10/150,262
 CURRENT FILING DATE: 2002-05-20
 PRIOR APPLICATION NUMBER: US/09/447,356
 PRIOR FILING DATE: 1999-11-22
 PRIOR APPLICATION NUMBER: 08/945,037
 PRIOR FILING DATE: 1998-01-12
 PRIOR APPLICATION NUMBER: GB 9508204.6
 PRIOR FILING DATE: 1995-04-21
 NUMBER OF SEQ ID NOS: 11
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 3
 LENGTH: 241
 TYPE: PRT
 ORGANISM: Murine sp.
 US-10-150-262-3

Query Match 100.0%; Score 1270; DB 9; Length 241;
 Best Local Similarity 100.0%; Pred. No. 2,3e-124;
 Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSMLFTLTITAFILGIGQAEPSHESNVPAGHTIPQVHWTKLOHSIDTLRRARSAAPAAIA 60
 Db 1 MSMLFTLTITAFILGIGQAEPSHESNVPAGHTIPQVHWTKLOHSIDTLRRARSAAPAAIA 60
 Qy 61 ARVAGOTRNTITVDPRLFKKRLRSRVLFSSTOPPREAADTODLDFEVGAAPFNRTTRSK 120
 Db 61 ARVAGOTRNTITVDPRLFKKRLRSRVLFSSTOPPREAADTODLDFEVGAAPFNRTTRSK 120
 Qy 121 RSSSHPIFHRGSEFVCDVSVMWGDKTTATDIDKGEVMVLGEVINNSVFQYFFETKCR 180
 Db 121 RSSSHPIFHRGSEFVCDVSVMWGDKTTATDIDKGEVMVLGEVINNSVFQYFFETKCR 180
 Qy 181 DPNPVDGCGRGIDSKMNSYCTTHTFVKALTMDSQAAMRFIRIDTACVLSKAVRR 240
 Db 181 DPNPVDGCGRGIDSKMNSYCTTHTFVKALTMDSQAAMRFIRIDTACVLSKAVRR 240
 Qy 241 A 241
 Db 241 A 241

RESULT 4
 US-10-155-886-1
 Sequence 1, Application US/10155886
 Publication No. US20030087804A1
 GENERAL INFORMATION:
 APPLICANT: Hempstead, Barbara L.
 APPLICANT: Lee, Ramee
 APPLICANT: Teng, Kenneth K.
 APPLICANT: Kernani, Pounch
 TITLE OF INVENTION: High Affinity Ligand For p75 Neurotrophin Receptor
 FILE REFERENCE: 955-21 Sequence No. US20030087804A1, 1-68
 CURRENT APPLICATION NUMBER: US/10/155,886
 CURRENT FILING DATE: 2002-08-05
 NUMBER OF SEQ ID NOS: 68

SOFTWARE: Patentin version 3.1
 SEQ ID NO 1
 LENGTH: 241
 TYPE: PRT
 ORGANISM: Homo sapien
 US-10-155-886-1

Query Match 100.0%; Score 1270; DB 9; Length 241;
 Best Local Similarity 100.0%; Pred. No. 2.3e-124;
 Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSMLFTLITAFLLIGIOAEPHSESNVPAAGHTIPQVHMTKLOHSLDTALRRASAPAAIA 60
 DB 1 MSMLFTLITAFLLIGIOAEPHSESNVPAAGHTIPQVHMTKLOHSLDTALRRASAPAAIA 60
 QY 61 ARVAGOTRNTITVDPRLFKKRLRSFVLSTQPPREAADTODLDFEVGAAPFNRTRSK 120
 DB 61 ARVAGOTRNTITVDPRLFKKRLRSFVLSTQPPREAADTODLDFEVGAAPFNRTRSK 120
 QY 121 RSSSHPIFRHGEFVCDVSVMVGDKTATDIDIKGEVMVLGEVINNSVFKQYFEETKCR 180
 DB 121 RSSSHPIFRHGEFVCDVSVMVGDKTATDIDIKGEVMVLGEVINNSVFKQYFEETKCR 180
 QY 181 DPNPVDSCGCGIDSKHNSYCTTHTFVKALTMDGKQAAWFRIRIDTACVLSRAVRR 240
 DB 181 DPNPVDSCGCGIDSKHNSYCTTHTFVKALTMDGKQAAWFRIRIDTACVLSRAVRR 240
 QY 241 A 241
 DB 241 A 241

RESULT 5

US-10-155-886-6
 Sequence 6, Application US/10155886
 Publication No. US20030087804A1
 GENERAL INFORMATION:

APPLICANT: Hemstead, Barbara L.
 APPLICANT: Lee, Kamee
 APPLICANT: Teng, Kenneth K.
 APPLICANT: Kermani, Pounesh
 TITLE OF INVENTION: High Affinity Ligand For p75 Neurotrophin Receptor
 FILE REFERENCE: 955-21 Sequence No US20030087804A1. 1-68
 CURRENT FILING DATE: 2002-08-05
 NUMBER OF SEQ ID NOS: 68
 SOFTWARE: Patentin version 3.1
 SEQ ID NO 6
 LENGTH: 241
 TYPE: PRT
 ORGANISM: Homo sapien
 US-10-155-886-6

Query Match 100.0%; Score 1270; DB 9; Length 241;
 Best Local Similarity 100.0%; Pred. No. 2.3e-124;
 Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSMLFTLITAFLLIGIOAEPHSESNVPAAGHTIPQVHMTKLOHSLDTALRRASAPAAIA 60
 DB 1 MSMLFTLITAFLLIGIOAEPHSESNVPAAGHTIPQVHMTKLOHSLDTALRRASAPAAIA 60
 QY 61 ARVAGOTRNTITVDPRLFKKRLRSFVLSTQPPREAADTODLDFEVGAAPFNRTRSK 120
 DB 61 ARVAGOTRNTITVDPRLFKKRLRSFVLSTQPPREAADTODLDFEVGAAPFNRTRSK 120
 QY 121 RSSSHPIFRHGEFVCDVSVMVGDKTATDIDIKGEVMVLGEVINNSVFKQYFEETKCR 180
 DB 121 RSSSHPIFRHGEFVCDVSVMVGDKTATDIDIKGEVMVLGEVINNSVFKQYFEETKCR 180
 QY 181 DPNPVDSCGCGIDSKHNSYCTTHTFVKALTMDGKQAAWFRIRIDTACVLSRAVRR 240
 DB 181 DPNPVDSCGCGIDSKHNSYCTTHTFVKALTMDGKQAAWFRIRIDTACVLSRAVRR 240

QY 241 A 241
 DB 241 A 241

RESULT 6

US-10-072-681-1
 Sequence 1, Application US/10072681
 Patent No. US20020137893A1
 GENERAL INFORMATION:

APPLICANT: Burton, Louis R.
 APPLICANT: Schmelzer, Charles H.
 APPLICANT: Beck, Joanne T.
 TITLE OF INVENTION: PURIFICATION OF NGF
 FILE REFERENCE: GENENT 037C3
 CURRENT FILING DATE: US/10/072,681
 CURRENT FILING DATE: 2002-02-08
 PRIOR APPLICATION NUMBER: 60/030838
 PRIOR FILING DATE: 1996-11-15
 PRIOR APPLICATION NUMBER: 60/047855
 PRIOR FILING DATE: 1997-05-29
 PRIOR APPLICATION NUMBER: 08/970865
 PRIOR FILING DATE: 1997-11-14
 PRIOR APPLICATION NUMBER: 09/363573
 PRIOR FILING DATE: 1999-07-29
 PRIOR APPLICATION NUMBER: 09/675,503
 PRIOR FILING DATE: 2000-09-29
 NUMBER OF SEQ ID NOS: 6
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 1
 LENGTH: 242
 TYPE: PRT
 ORGANISM: Homo sapien
 US-10-072-681-1

Query Match 100.0%; Score 1270; DB 12; Length 242;
 Best Local Similarity 100.0%; Pred. No. 2.3e-124;
 Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSMLFTLITAFLLIGIOAEPHSESNVPAAGHTIPQVHMTKLOHSLDTALRRASAPAAIA 60
 DB 2 MSMLFTLITAFLLIGIOAEPHSESNVPAAGHTIPQVHMTKLOHSLDTALRRASAPAAIA 61
 QY 61 ARVAGOTRNTITVDPRLFKKRLRSFVLSTQPPREAADTODLDFEVGAAPFNRTRSK 120
 DB 62 ARVAGOTRNTITVDPRLFKKRLRSFVLSTQPPREAADTODLDFEVGAAPFNRTRSK 121
 QY 121 RSSSHPIFRHGEFVCDVSVMVGDKTATDIDIKGEVMVLGEVINNSVFKQYFEETKCR 180
 DB 122 RSSSHPIFRHGEFVCDVSVMVGDKTATDIDIKGEVMVLGEVINNSVFKQYFEETKCR 181
 QY 181 DPNPVDSCGCGIDSKHNSYCTTHTFVKALTMDGKQAAWFRIRIDTACVLSRAVRR 240
 DB 182 DPNPVDSCGCGIDSKHNSYCTTHTFVKALTMDGKQAAWFRIRIDTACVLSRAVRR 241
 QY 241 A 241
 DB 242 A 242

RESULT 7

US-09-822-263-16
 Sequence 16, Application US/09822263
 Patent No. US20020036598A1
 GENERAL INFORMATION:

APPLICANT: Prayaga, Sudhirdas
 APPLICANT: Vernet, Corine
 APPLICANT: Shinkete, Richard A
 APPLICANT: Burgess, Catherine
 APPLICANT: Spytek, Kimberly
 APPLICANT: Tchernyev, Velizar T
 TITLE OF INVENTION: No. US20020036598A1el Polynucleotides and Polypeptides Encoded T
 FILE REFERENCE: 15966-572 C1P1

```

/ CURRENT APPLICATION NUMBER: US/09/822,263
/ CURRENT FILING DATE: 2001-06-15
/ PRIOR APPLICATION NUMBER: 09/672,665
/ PRIOR FILING DATE: 2000-09-28
/ PRIOR APPLICATION NUMBER: 60/156,745
/ PRIOR FILING DATE: 1999-09-30
/ PRIOR APPLICATION NUMBER: 60/158,942
/ PRIOR FILING DATE: 1998-10-06
/ PRIOR APPLICATION NUMBER: 60/159,248
/ PRIOR FILING DATE: 1999-10-13
/ PRIOR APPLICATION NUMBER: 60/169,344
/ PRIOR FILING DATE: 1999-12-06
/ PRIOR APPLICATION NUMBER: 60/215,048
/ PRIOR FILING DATE: 2000-06-29
/ NUMBER OF SEQ ID NOS: 36
/ SOFTWARE: Patent In Ver. 2.1
/ SEQ ID NO 16
/ LENGTH: 241
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-822-263-16

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Query Match          99.7%; Score 1266; DB 10; Length 241;
Best Local Similarity 99.6%; Pred. No. 6e-124;
Matches 240; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSMLFYLITLTAFLIGIOAEPHSESNVPAGHTIPQVHTKLOHSLDTALRRARSAPAAIA 60
DB 1 MSMLFYLITLTAFLIGIOAEPHSESNVPAGHTIPQVHTKLOHSLDTALRRARSAPAAIA 60
QY 61 ARVAGQTNITVDRLFKKRLRSPRLVFTSTOPPREADTODLDFEVGAAPFNRTTRSK 120
DB 61 ARVAGQTNITVDRLFKKRLRSPRLVFTSTOPPREADTODLDFEVGAAPFNRTTRSK 120
QY 121 RSSSHPIFRGGEFVSCDSVWVGDKTTATDIDKGEVWVLGEVINNSVFKQYFEETKCR 180
DB 121 RSSSHPIFRGGEFVSCDSVWVGDKTTATDIDKGEVWVLGEVINNSVFKQYFEETKCR 180
QY 181 DPNPVDGCGRGIDSKHNSYCTTHTTFVKALTMDGKQAAARFIRIDTACVLSRKAVER 240
DB 181 DPNPVDGCGRGIDSKHNSYCTTHTTFVKALTMDGKQAAARFIRIDTACVLSRKAVER 240
QY 241 A 241
DB 241 A 241

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RESULT 8
US-09-788-188-2
/ Sequence 2, Application US/09788188
/ Publication No. US20030040082A1
/ GENERAL INFORMATION:
/ APPLICANT: TUSZYNSKI, MARK
/ APPLICANT: BLESCH, ARMTN
/ TITLE OF INVENTION: MUTANT PRO-NEUROTROPHIN WITH IMPROVED ACTIVITY
/ FILE REFERENCE: 041673/2045
/ CURRENT APPLICATION NUMBER: US/09/788,188
/ CURRENT FILING DATE: 2001-02-16
/ NUMBER OF SEQ ID NOS: 16
/ SOFTWARE: Patent In Ver. 2.1
/ SEQ ID NO 2
/ LENGTH: 241
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Mutant NGF
/ OTHER INFORMATION: pro-neurotrophin
US-09-788-188-2

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Query Match          99.6%; Score 1265; DB 9; Length 241;
Best Local Similarity 99.6%; Pred. No. 7.6e-124;
Matches 240; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MSMLFYLITLTAFLIGIOAEPHSESNVPAGHTIPQVHTKLOHSLDTALRRARSAPAAIA 60
DB 1 MSMLFYLITLTAFLIGIOAEPHSESNVPAGHTIPQVHTKLOHSLDTALRRARSAPAAIA 60
QY 61 ARVAGQTNITVDRLFKKRLRSPRLVFTSTOPPREADTODLDFEVGAAPFNRTTRSK 120
DB 61 ARVAGQTNITVDRLFKKRLRSPRLVFTSTOPPREADTODLDFEVGAAPFNRTTRSK 120
QY 121 RSSSHPIFRGGEFVSCDSVWVGDKTTATDIDKGEVWVLGEVINNSVFKQYFEETKCR 180
DB 121 RSSSHPIFRGGEFVSCDSVWVGDKTTATDIDKGEVWVLGEVINNSVFKQYFEETKCR 180
QY 181 DPNPVDGCGRGIDSKHNSYCTTHTTFVKALTMDGKQAAARFIRIDTACVLSRKAVER 240
DB 181 DPNPVDGCGRGIDSKHNSYCTTHTTFVKALTMDGKQAAARFIRIDTACVLSRKAVER 240
QY 241 A 241
DB 241 A 241

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RESULT 9
US-10-155-886-7
/ Sequence 7, Application US/10155886
/ Publication No. US20030087804A1
/ GENERAL INFORMATION:
/ APPLICANT: Hempstead, Barbara L.
/ APPLICANT: Lee, Ramona K.
/ APPLICANT: Teng, Kenneth K.
/ TITLE OF INVENTION: High Affinity Ligand For p75 Neurotrophin Receptor
/ FILE REFERENCE: 955-21 Sequence No. US20030087804A1. 1-68
/ CURRENT APPLICATION NUMBER: US/10/155,886
/ CURRENT FILING DATE: 2002-08-05
/ NUMBER OF SEQ ID NOS: 68
/ SOFTWARE: Patent In version 3.1
/ SEQ ID NO 7
/ LENGTH: 241
/ TYPE: PRT
/ ORGANISM: Gorilla gorilla
US-10-155-886-7

```

```

Query Match          98.3%; Score 1249; DB 9; Length 241;
Best Local Similarity 98.8%; Pred. No. 3.6e-122;
Matches 238; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MSMLFYLITLTAFLIGIOAEPHSESNVPAGHTIPQVHTKLOHSLDTALRRARSAPAAIA 60
DB 1 MSMLFYLITLTAFLIGIOAEPHSESNVPAGHTIPQVHTKLOHSLDTALRRARSAPAAIA 60
QY 61 ARVAGQTNITVDRLFKKRLRSPRLVFTSTOPPREADTODLDFEVGAAPFNRTTRSK 120
DB 61 ARVAGQTNITVDRLFKKRLRSPRLVFTSTOPPREADTODLDFEVGAAPFNRTTRSK 120
QY 121 RSSSHPIFRGGEFVSCDSVWVGDKTTATDIDKGEVWVLGEVINNSVFKQYFEETKCR 180
DB 121 RSSSHPIFRGGEFVSCDSVWVGDKTTATDIDKGEVWVLGEVINNSVFKQYFEETKCR 180
QY 181 DPNPVDGCGRGIDSKHNSYCTTHTTFVKALTMDGKQAAARFIRIDTACVLSRKAVER 240
DB 181 DPNPVDGCGRGIDSKHNSYCTTHTTFVKALTMDGKQAAARFIRIDTACVLSRKAVER 240
QY 241 A 241
DB 241 A 241

```

```

RESULT 10
US-10-155-886-8
/ Sequence 8, Application US/10155886
/ Publication No. US20030087804A1
/ GENERAL INFORMATION:
/ APPLICANT: Hempstead, Barbara L.

```

```

APPLICANT: Lee, Ramee
APPLICANT: Teng, Kenneth K.
APPLICANT: Kernani, Pouneh
TITLE OF INVENTION: High Affinity Ligand For p75 Neurotrophin Receptor
FILE REFERENCE: 955-21 Sequence No. US20030087804A1. 1-68
CURRENT APPLICATION NUMBER: US/10/155, 886
CURRENT FILING DATE: 2002-08-05
NUMBER OF SEQ ID NOS: 68
SOFTWARE: PatentIn version 3.1
SEQ ID NO 8
LENGTH: 241
TYPE: PRT
ORGANISM: Rattus norvegicus
US-10-155-886-8

Query Match      87.2%; Score 1107, DB 9; Length 241;
Best Local Similarity 85.8%; Pred. No. 2,3e-107;
Matches 206; Conservative 14; Mismatches 20; Indels 0; Gaps 0;

1 MSMLPYTITATLVLIGIOAEPHSESVPNGHTIPQVHWTKLOHSLDTLRLRRASAPAAALIA 60
1 MSMLPYTITATLVLIGIOAEPHSESVPNGHSDSVPEAHWTLOHSLDTLRLRRASAPAAALIA 60
1 ARVAGQTNITVDPLPKKRLRSRVLFTSTPPREAADTODLDFEVGAAPFNRTHSK 120
61 ARVAGQTNITVDPLPKKRLRSRVLFTSTPPREAADTODLDFEVGAAPFNRTHSK 120
61 ARVAGQTNITVDPLPKKRLRSRVLFTSTPPREAADTODLDFEVGAAPFNRTHSK 120
121 RSSHPITRHGRFSCDSVSWVGDKTTATDIDKGEVWVLGEVINNSVFKQYFFETKCR 180
121 RSSHPITRHGRFSCDSVSWVGDKTTATDIDKGEVWVLGEVINNSVFKQYFFETKCR 180
121 RSSHPITRHGRFSCDSVSWVGDKTTATDIDKGEVWVLGEVINNSVFKQYFFETKCR 180
181 DPNPDSGCRGIDSGHNSYCTTHTFVKALTMOSKOAAEPIRDPKCVCLSRKAVR 240
181 DPNPDSGCRGIDSGHNSYCTTHTFVKALTMOSKOAAEPIRDPKCVCLSRKAVR 240
181 APNPESGCRGIDSGHNSYCTTHTFVKALTMOSKOAAEPIRDPKCVCLSRKAVR 240

RESULT 11
US-10-155-886-10
Sequence 10, Application US/10155886
Publication No. US20030087804A1
GENERAL INFORMATION:
APPLICANT: Hempstead, Barbara L.
APPLICANT: Lee, Ramee
APPLICANT: Teng, Kenneth K.
APPLICANT: Kernani, Pouneh
TITLE OF INVENTION: High Affinity Ligand For p75 Neurotrophin Receptor
FILE REFERENCE: 955-21 Sequence No. US20030087804A1. 1-68
CURRENT APPLICATION NUMBER: US/10/155, 886
CURRENT FILING DATE: 2002-08-05
NUMBER OF SEQ ID NOS: 68
SOFTWARE: PatentIn version 3.1
SEQ ID NO 10
LENGTH: 231
TYPE: PRT
ORGANISM: Bos taurus
US-10-155-886-10

Query Match      87.1%; Score 1106, DB 9; Length 231;
Best Local Similarity 90.7%; Pred. No. 2,7e-107;
Matches 205; Conservative 7; Mismatches 14; Indels 0; Gaps 0;

1 AFLIGIOAEPHSESVPNGHTIPQVHWTKLOHSLDTLRLRRASAPAAALIAARVAGQTNIT 70
1 AFLIGIOAEPHSESVPNGHTIPQVHWTKLOHSLDTLRLRRASAPAAALIAARVAGQTNIT 70
1 AFLIGIOAEPHSESVPNGHTIPQVHWTKLOHSLDTLRLRRASAPAAALIAARVAGQTNIT 70
71 TNDPLPKKRLRSRVLFTSTPPREAADTODLDFEVGAAPFNRTHSKSSGHP1FHR 130
71 TNDPLPKKRLRSRVLFTSTPPREAADTODLDFEVGAAPFNRTHSKSSGHP1FHR 130
61 TNDPLPKKRLRSRVLFTSTPPREAADTODLDFEVGAAPFNRTHSKSSGHP1FHR 120
131 GEFVCDVSVWVGDKTTATDIDKGEVWVLGEVINNSVFKQYFFETKCRDPNPVDSGCR 190
131 GEFVCDVSVWVGDKTTATDIDKGEVWVLGEVINNSVFKQYFFETKCRDPNPVDSGCR 190
121 GEFVCDVSVWVGDKTTATDIDKGEVWVLGEVINNSVFKQYFFETKCRDPNPVDSGCR 180

```

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Qy      191 GIDSKMNSYCTTHTEFVALTMDGQAMRFRIIDTACVLSRK 236
      |||
Db      181 GIDAKMNSYCTTHTEFVALTMDGQAMRFRIIDTACVLSRK 226

RESULT 12
US-10-155-886-9
; Sequence 9, Application US/10155886
; Publication No. US20030087804A1
; GENERAL INFORMATION:
; APPLICANT: Hempstead, Barbara L.
; APPLICANT: Lee, Kamee
; APPLICANT: Teng, Kenneth K.
; TITLE OF INVENTION: High Affinity Ligand For p75 Neurotrophin Receptor
; FILE REFERENCE: 955-21 Sequence No. US20030087804A1. 1-68
; CURRENT APPLICATION NUMBER: US/10/155,886
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-155-886-9

Query Match      86.3%; Score 1096; DB 9; Length 241;
Best Local Similarity 85.0%; Pred. No. 3,2e-106;
Matches 204; Conservative 14; Mismatches 22; Indels 0; Gaps 0

Qy      1 MSMFTYTLITAFLLGIGQAEPHSESNVPAAGHTIPQVHWTKLQHSIDTALRRARSAPAAIA 60
      |||
Db      1 MSMFTYTLITAFLLGIGQAEPTDSVPEGDSVPEAHWTKLQHSIDTALRRARSAPTAEIA 60

Qy      61 ARVAGQTNITVDRLPEKRLRSPRYLFSNOPREABDODLDEVEGGAPEPNTTHSK 120
      |||
Db      61 ARVAGQTNITVDRLPEKRLRSHRYLFSNOPREABDODLDEVEGGAPEPNTTHSK 120

Qy      121 RSSSHPIFRHGEFSVCDVSVMVGDKTATDIIKKEVWVLGEVININNSVFQYFPETKCR 180
      |||
Db      121 RSSTHPIVHMGFEFSVCDVSVMVGDKTATDIIKKEVYVLAIVININNSVFQYFPETKCR 180

Qy      181 DPNVDSGCRGIDSKHMNSYCTTHTEFVALTMDGQAMRFRIIDTACVLSRKAVR 240
      |||
Db      181 ASNVESEGCRGIDSKHMNSYCTTHTEFVALTMDGQAMRFRIIDTACVLSRKATR 240

RESULT 13
US-10-155-886-11
; Sequence 11, Application US/10155886
; Publication No. US20030087804A1
; GENERAL INFORMATION:
; APPLICANT: Hempstead, Barbara L.
; APPLICANT: Lee, Kamee
; APPLICANT: Teng, Kenneth K.
; APPLICANT: Kermant, Pouneh
; TITLE OF INVENTION: High Affinity Ligand For p75 Neurotrophin Receptor
; FILE REFERENCE: 955-21 Sequence No. US20030087804A1. 1-68
; CURRENT APPLICATION NUMBER: US/10/155,886
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Gallus gallus
US-10-155-886-11

Query Match      62.1%; Score 788.5; DB 9; Length 243;
Best Local Similarity 64.9%; Pred. No. 3.7e-74;
Matches 161; Conservative 20; Mismatches 48; Indels 19; Gaps 6;

Qy      1 MSMFTYTLITAFLLGIGQAEPHSESN---VPAGHTIPQVHWTKLQHSIDTALRRARSAPA 56

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Db      5  MSMLYTLITLITAFIGQAAPKSEDNQPLEYPAHSHSPSTQOSGQHT-----AQAAPQ 57
Qy      57  AATAAFA-----GQFRNITVDRLFKRRLSPVLFSTQPREADTODLDFEVGA 111
Db      58  TT-HGFAPWPDGTEDLNIAMDQNFKKRFRSSRLVFGTQPPVSRKQSTGCF-LSSAV 115
Qy      112  PPRTRRSRSSHPIFHNGEFSVCDSVWVGDKTATDIDKGEVWLGEVNNINSVFK 171
Db      116  SLNRTRATRR-TNHPVLHNGEFSVCDSVWVGDKTATDIDKGEVWLGEVNNINSVFK 174
Qy      172  QYFETKCRDPNPVDSGCRGIDSKHNSYCTTHTFVKALTMDSQAAMRFIRIDTACVC 231
Db      175  QYFETKCRDPNPVDSGCRGIDSKHNSYCTTHTFVKALTMDSQAAMRFIRIDTACVC 234
Qy      232  VLSRAVR 239
Db      235  VLSRSGR 242

```

```

RESULT 14
US-10-155-886-12
; Sequence 12, Application US/10155886
; Publication No. US20030087804A1
; GENERAL INFORMATION:
; APPLICANT: Hemstead, Barbara L.
; APPLICANT: Lee, Ramee
; APPLICANT: Teng, Kenneth K.
; APPLICANT: Kermani, Pounah
; TITLE OF INVENTION: High Affinity Ligand For p75 Neurotrophin Receptor
; FILE REFERENCE: 955-21 Sequence No. US20030087804A1. 1-68
; CURRENT FILING DATE: 2002-08-05
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Xenopus laevis
US-10-155-886-12

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Query Match      60.9%; Score 773; DB 9; Length 235;
Best Local Similarity 63.6%; Pred. No. 1.5e-72;
Matches 154; Conservative 27; Mismatches 41; Indels 20; Gaps 6;

Qy      1  MSMLYTLITLITAFIGQAAPKSEDNQPLEYPAHSHSPSTQOSGQHT-----AQAAPQ 54
Db      5  MSMLYTLITLITAFIGQAAPKSEDNQPLEYPAHSHSPSTQOSGQHT-----AQAAPQ 53
Qy      55  PAAAIARVAGQNTNITVDRLFKRRLSPVLFSTQPREADTODLDFEVGAAPFN 114
Db      54  -HGTLBAKEPSYFNNVTVDPFLFRKRFRSPVLFSTQPPLESDFOHLEY-LDDESLN 111
Qy      115  RTHSRKSSSHPIFHNGEFSVCDSVWVGDKTATDIDKGEVWLGEVNNINSVFKOYF 174
Db      112  KTIIPAKR-TVHPVLHNGEFSVCDSVWVGDKTATDIDKGEVWLGEVNNINSVFKOYF 170
Qy      175  FETKCRDPNPVDSGCRGIDSKHNSYCTTHTFVKALTMDSQAAMRFIRIDTACVCVL 234
Db      171  FETKCRDPNPVDSGCRGIDSKHNSYCTTHTFVKALTMDSQAAMRFIRIDTACVCVL 230
Qy      235  RK 236
Db      231  RK 232

```

```

RESULT 15
US-10-150-262-1
; Sequence 1, Application US/10150262
; Publication No. US20030049264A1
; GENERAL INFORMATION:
; APPLICANT: FOSTER, KEITH ALAN
; APPLICANT: DUGGAN, MICHAEL JOHN

```

```

; APPLICANT: SHONE, CLIFFORD CHARLES
; TITLE OF INVENTION: CLOSTRIDIAL TOXIN DERIVATIVES ABLE TO MODIFY
; TITLE OF INVENTION: PERIPHERAL
; FILE REFERENCE: 023223/0104
; CURRENT FILING DATE: 2002-05-20
; PRIOR FILING DATE: 1999-11-22
; PRIOR APPLICATION NUMBER: US/09/447,356
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: GB 9508204.6
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Murine sp.
US-10-150-262-1

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Query Match      51.3%; Score 651; DB 9; Length 120;
Best Local Similarity 100.0%; Pred. No. 3e-60;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      122  SSSHPFHRGSEFSVCDSVWVGDKTATDIDKGEVWLGEVNNINSVFKOYFETKCRD 181
Db      1  SSSHPFHRGSEFSVCDSVWVGDKTATDIDKGEVWLGEVNNINSVFKOYFETKCRD 60
Qy      182  PNPVDSGCRGIDSKHNSYCTTHTFVKALTMDSQAAMRFIRIDTACVCVLSRAVARA 241
Db      61  PNPVDSGCRGIDSKHNSYCTTHTFVKALTMDSQAAMRFIRIDTACVCVLSRAVARA 120

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Search completed: June 6, 2003, 10:52:46
 Job time : 18.5 secs

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OM protein - protein search, using sw model

Run on: June 6, 2003, 10:48:22 ; Search time 12.5 Seconds
(without alignments)
567.274 Million cell updates/sec

Title: US-09-788-188-1

Perfect score: 1270
Sequence: 1 MSMLFYLITRAFLIGIQAE.....FIRIDTACVLSRRKAVRA 241

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Issued Patente AA.*
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep.*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/PTGUS.COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1270	100.0	241	1	US-08-266-080B-4
2	1270	100.0	241	1	US-08-451-947-5
3	1270	100.0	241	2	US-08-424-826A-5
4	1270	100.0	241	2	US-08-595-043A-75
5	1270	100.0	241	3	US-08-970-865-1
6	1270	100.0	241	3	US-08-928-694-5
7	1270	100.0	241	4	US-09-363-573-1
8	1270	100.0	241	4	US-09-447-356-3
9	1270	100.0	241	5	PCT-US91-06950-5
10	1270	100.0	241	5	PCT-US95-05423-4
11	1270	100.0	242	4	US-09-675-503-1
12	996	78.4	240	3	US-08-910-691-11
13	651	51.3	120	1	US-08-440-049-3
14	651	51.3	120	2	US-08-441-513A-3
15	651	51.3	120	3	US-08-581-662-31
16	651	51.3	120	4	US-08-845-541B-1
17	651	51.3	120	4	US-09-066-065A-1
18	651	51.3	120	4	US-09-447-356-1
19	651	51.3	120	4	US-09-664-295-31
20	651	51.3	120	5	PCT-US95-06918-3
21	648	51.0	120	3	US-08-970-865-2
22	648	51.0	120	4	US-09-363-573-2
23	648	51.0	121	4	US-09-675-503-2
24	648	51.0	157	4	US-09-675-922-4
25	647.5	51.0	167	4	US-09-675-922-8
26	642	50.6	119	3	US-08-753-642-2
27	642	50.6	153	4	US-09-675-922-2

28	642	50.6	163	4	US-09-675-922-6	Sequence 6, Appl1
29	637	50.2	120	4	US-08-845-541B-3	Sequence 3, Appl1
30	637	50.2	120	4	US-09-066-065A-3	Sequence 3, Appl1
31	634	49.9	120	4	US-08-845-541B-4	Sequence 4, Appl1
32	634	49.9	120	4	US-09-066-065A-4	Sequence 4, Appl1
33	629	49.5	120	4	US-08-845-541B-12	Sequence 12, Appl1
34	629	49.5	120	4	US-09-066-065A-12	Sequence 12, Appl1
35	628	49.4	120	4	US-08-845-541B-17	Sequence 17, Appl1
36	628	49.4	120	4	US-08-845-541B-20	Sequence 20, Appl1
37	628	49.4	120	4	US-09-066-065A-17	Sequence 17, Appl1
38	628	49.4	120	4	US-09-066-065A-20	Sequence 20, Appl1
39	626	49.3	120	4	US-08-845-541B-21	Sequence 21, Appl1
40	626	49.3	120	4	US-09-066-065A-18	Sequence 18, Appl1
41	626	49.3	120	4	US-09-066-065A-21	Sequence 21, Appl1
42	626	49.3	120	4	US-08-845-541B-13	Sequence 13, Appl1
43	623	49.1	120	4	US-08-845-541B-19	Sequence 19, Appl1
44	623	49.1	120	4	US-09-066-065A-13	Sequence 13, Appl1
45	623	49.1	120	4	US-09-066-065A-13	Sequence 13, Appl1

ALIGNMENTS

RESULT 1
US-08-266-080B-4
Sequence 4, Application US/08266080B
Patent No. 5606031
GENERAL INFORMATION:
APPLICANT: Jack Lile
APPLICANT: Tadahiko Kohno
APPLICANT: Duane Bonam
TITLE OF INVENTION: Production of Biologically Active
TITLE OF INVENTION: Recombinant Neurotrophic Protein
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/266,080B
FILING DATE: 27-JUNE-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/240,122
FILING DATE: 09-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/087,912
FILING DATE: 06-JULY-1993
APPLICATION DATA:
FILING DATE: 04-APRIL-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/594,126
FILING DATE: 09-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/547,750
FILING DATE: 02-JULY-1990
APPLICATION DATA:
APPLICATION NUMBER: 07/505,441
FILING DATE: 06-APRIL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: SYNE200C5
TELECOMMUNICATION INFORMATION:

TELEPHONE: (303) 793-3333
 TELEFAX: (303) 793-3433
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 241 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 FEATURE:
 NAME/KEY: inferred amino acid sequence of human NGF
 US-08-266-0808-4

Query Match 100.0%; Score 1270; DB 1; Length 241;
 Best Local Similarity 100.0%; Pred. No. 1.1e-142; Indels 0; Gaps 0;
 Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSMLFYTLITAPLIGIOAEPHSESNVPAGHTIPQVHTKLOHSLDTALRRASAPAAIA 60
 DB 1 MSMLFYTLITAPLIGIOAEPHSESNVPAGHTIPQVHTKLOHSLDTALRRASAPAAIA 60
 QY 61 ARVAGQTRNITVDPRLPFKKRLRSRVLFTSTPPREADTODLDFEVGAAPFNRTTRSK 120
 DB 61 ARVAGQTRNITVDPRLPFKKRLRSRVLFTSTPPREADTODLDFEVGAAPFNRTTRSK 120
 QY 121 RSSSHPIFRHGEFSVCDVSVMWGDKTATDIDKGEVMVLGEVINNSVFKQYFFETKCR 180
 DB 121 RSSSHPIFRHGEFSVCDVSVMWGDKTATDIDKGEVMVLGEVINNSVFKQYFFETKCR 180
 QY 181 DENPVDSGCRGIDSKHNSYCTTHTFVKALTMDGKQAMRFIRIDTACVLSRAVRR 240
 DB 181 DENPVDSGCRGIDSKHNSYCTTHTFVKALTMDGKQAMRFIRIDTACVLSRAVRR 240
 QY 241 A 241
 DB 241 A 241

RESULT 2

US-08-451-947-5
 Sequence 5, Application us/08451947
 Patent No. 5702906
 GENERAL INFORMATION:
 APPLICANT: GENE TECH, INC.
 TITLE OF INVENTION: NOVEL NEUROTROPHIC FACTOR
 NUMBER OF SEQUENCES: 100
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 460 Point San Bruno Blvd
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: patin (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/451,947
 FILING DATE:
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/426419
 FILING DATE: 19-APR-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/030013
 FILING DATE: 22-MAR-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/648482
 FILING DATE: 31-JAN
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/587707
 FILING DATE: 1991

ATTORNEY/AGENT INFORMATION:
 NAME: Torchia, Timothy E.
 REGISTRATION NUMBER: 36,700
 REFERENCE/DOCKET NUMBER: 666P2CID2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415/952-8674
 TELEFAX: 415/952-8881
 TELERX: 910/371-7168
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 241 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 US-08-451-947-5

Query Match 100.0%; Score 1270; DB 1; Length 241;
 Best Local Similarity 100.0%; Pred. No. 1.1e-142; Indels 0; Gaps 0;
 Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSMLFYTLITAPLIGIOAEPHSESNVPAGHTIPQVHTKLOHSLDTALRRASAPAAIA 60
 DB 1 MSMLFYTLITAPLIGIOAEPHSESNVPAGHTIPQVHTKLOHSLDTALRRASAPAAIA 60
 QY 61 ARVAGQTRNITVDPRLPFKKRLRSRVLFTSTPPREADTODLDFEVGAAPFNRTTRSK 120
 DB 61 ARVAGQTRNITVDPRLPFKKRLRSRVLFTSTPPREADTODLDFEVGAAPFNRTTRSK 120
 QY 121 RSSSHPIFRHGEFSVCDVSVMWGDKTATDIDKGEVMVLGEVINNSVFKQYFFETKCR 180
 DB 121 RSSSHPIFRHGEFSVCDVSVMWGDKTATDIDKGEVMVLGEVINNSVFKQYFFETKCR 180
 QY 181 DENPVDSGCRGIDSKHNSYCTTHTFVKALTMDGKQAMRFIRIDTACVLSRAVRR 240
 DB 181 DENPVDSGCRGIDSKHNSYCTTHTFVKALTMDGKQAMRFIRIDTACVLSRAVRR 240
 QY 241 A 241
 DB 241 A 241

RESULT 3

US-08-424-826A-5
 Sequence 5, Application US/08424826A
 Patent No. 5830858
 GENERAL INFORMATION:
 APPLICANT: Rosenthal, Arnon
 TITLE OF INVENTION: NOVEL NEUROTROPHIC FACTOR
 NUMBER OF SEQUENCES: 98
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 460 Point San Bruno Blvd
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WinPatIn (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/424,826A
 FILING DATE: 19-APR-1995
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/240387
 FILING DATE: 10-MAY-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/648482
 FILING DATE: 31-JAN-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/587707
 FILING DATE: 25-SEP-1990

ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Ph.D., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P0666PIC2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-8674
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 241 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear

US-08-424-826A-5

Query Match 100.0%; Score 1270; DB 2; Length 241;
Best Local Similarity 100.0%; Pred. No. 1.1e-142;
Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSMLFTLLTAFLIGIOAEPSHSNVPAGHTTPOVHWTLOHSLDTALRRASAPAAATA 60
DB 1 MSMLFTLLTAFLIGIOAEPSHSNVPAGHTTPOVHWTLOHSLDTALRRASAPAAATA 60
QY 61 ARVAGQTRNITVDPLFKKRLRSPVLFSTOPPREAADTODLDFEVGGAAPFNRTTRSK 120
DB 61 ARVAGQTRNITVDPLFKKRLRSPVLFSTOPPREAADTODLDFEVGGAAPFNRTTRSK 120
QY 121 RSSSHPIFRGFSVCDVSVMVGDKTTATDIKKEVWVLGEVNNINSVFKQYFFETKCR 180
DB 121 RSSSHPIFRGFSVCDVSVMVGDKTTATDIKKEVWVLGEVNNINSVFKQYFFETKCR 180
QY 181 DPNPVDGCGRGIDSKHNSYCTTHTFVKALTMQKQAMFIRIDTACVCLSKAVR 240
DB 181 DPNPVDGCGRGIDSKHNSYCTTHTFVKALTMQKQAMFIRIDTACVCLSKAVR 240
QY 241 A 241
DB 241 A 241

RESULT 4

US-08-595-043A-75
Sequence 75, Application US/08595043A
Patent No. 5935824
GENERAL INFORMATION:
APPLICANT: SGARLATO, GREGORY D.
TITLE OF INVENTION: PROTEIN EXPRESSION SYSTEM
NUMBER OF SEQUENCES: 90
CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL
STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/595,043A
FILING DATE: 31-JAN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: SGAR-00371
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 75:
SEQUENCE CHARACTERISTICS:

LENGTH: 241 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULAR TYPE: protein
US-08-595-043A-75

Query Match 100.0%; Score 1270; DB 2; Length 241;
Best Local Similarity 100.0%; Pred. No. 1.1e-142;
Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSMLFTLLTAFLIGIOAEPSHSNVPAGHTTPOVHWTLOHSLDTALRRASAPAAATA 60
DB 1 MSMLFTLLTAFLIGIOAEPSHSNVPAGHTTPOVHWTLOHSLDTALRRASAPAAATA 60
QY 61 ARVAGQTRNITVDPLFKKRLRSPVLFSTOPPREAADTODLDFEVGGAAPFNRTTRSK 120
DB 61 ARVAGQTRNITVDPLFKKRLRSPVLFSTOPPREAADTODLDFEVGGAAPFNRTTRSK 120
QY 121 RSSSHPIFRGFSVCDVSVMVGDKTTATDIKKEVWVLGEVNNINSVFKQYFFETKCR 180
DB 121 RSSSHPIFRGFSVCDVSVMVGDKTTATDIKKEVWVLGEVNNINSVFKQYFFETKCR 180
QY 181 DPNPVDGCGRGIDSKHNSYCTTHTFVKALTMQKQAMFIRIDTACVCLSKAVR 240
DB 181 DPNPVDGCGRGIDSKHNSYCTTHTFVKALTMQKQAMFIRIDTACVCLSKAVR 240
QY 241 A 241
DB 241 A 241

RESULT 5

US-08-970-865-1
Sequence 1, Application US/08970865
Patent No. 6005081
GENERAL INFORMATION:
APPLICANT: Louis E. Burton, Charles H. Schmeizler, Joanne T. Beck
TITLE OF INVENTION: Purification of NGF
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/970,865
FILING DATE: 14-NOV-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/030838
FILING DATE: 11/15/1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/047855
FILING DATE: 5/29/1997
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Ph.D., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1063R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 241 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear

US-08-970-865-1

Query Match 100.0%; Score 1270; DB 3; Length 241;
Best Local Similarity 100.0%; Pred. No. 1,1e-142;
Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSMLFYTLITAFILGIGQAEPSHESNVPAGHTIPQVHTKLOHSIDLTLRRASAPAAIA 60
DB 1 MSMLFYTLITAFILGIGQAEPSHESNVPAGHTIPQVHTKLOHSIDLTLRRASAPAAIA 60
QY 61 ARVAGOTRNTITVDPRLFKKRLRSRVLFTSTOPPREADODDLFEVGGAAPFRTTRSK 120
DB 61 ARVAGOTRNTITVDPRLFKKRLRSRVLFTSTOPPREADODDLFEVGGAAPFRTTRSK 120
QY 121 RSSSHPIFRHGEFSCDSVSVMVGDKTTATIDIKGEVWVLGEVNNINSVFQYFEETKCR 180
DB 121 RSSSHPIFRHGEFSCDSVSVMVGDKTTATIDIKGEVWVLGEVNNINSVFQYFEETKCR 180
QY 181 DPNPVDGCGRGIDSKHNSYCTTHTFVKALTMGQQAAMRFIRIDTACVLSRKAARR 240
DB 181 DPNPVDGCGRGIDSKHNSYCTTHTFVKALTMGQQAAMRFIRIDTACVLSRKAARR 240
QY 241 A 241
DB 241 A 241

RESULT 6

US-08-928-694-5
Sequence 5, Application US/08928694
Patent No. 6037320

GENERAL INFORMATION:

APPLICANT: ROSENTHAL, ARNON
TITLE OF INVENTION: NOVEL NEUROTROPHIC FACTOR
NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,694
FILING DATE: 12-Sep-1997

CLASSIFICATION: 424

PRIOR APPLICATION: 424
APPLICATION NUMBER: 08/451947
FILING DATE: 26-MAY-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/424419
FILING DATE: 19-APR-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/030013
FILING DATE: 22-MAR-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/648482
FILING DATE: 31-JAN

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/587707
FILING DATE: 1991

ATTORNEY/AGENT INFORMATION:
NAME: Torchia, PhD., Timothy E.

REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P0666P2C1D2C1

TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:
LENGTH: 241 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear

US-08-928-694-5

Query Match 100.0%; Score 1270; DB 3; Length 241;
Best Local Similarity 100.0%; Pred. No. 1,1e-142;
Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSMLFYTLITAFILGIGQAEPSHESNVPAGHTIPQVHTKLOHSIDLTLRRASAPAAIA 60
DB 1 MSMLFYTLITAFILGIGQAEPSHESNVPAGHTIPQVHTKLOHSIDLTLRRASAPAAIA 60
QY 61 ARVAGOTRNTITVDPRLFKKRLRSRVLFTSTOPPREADODDLFEVGGAAPFRTTRSK 120
DB 61 ARVAGOTRNTITVDPRLFKKRLRSRVLFTSTOPPREADODDLFEVGGAAPFRTTRSK 120
QY 121 RSSSHPIFRHGEFSCDSVSVMVGDKTTATIDIKGEVWVLGEVNNINSVFQYFEETKCR 180
DB 121 RSSSHPIFRHGEFSCDSVSVMVGDKTTATIDIKGEVWVLGEVNNINSVFQYFEETKCR 180
QY 181 DPNPVDGCGRGIDSKHNSYCTTHTFVKALTMGQQAAMRFIRIDTACVLSRKAARR 240
DB 181 DPNPVDGCGRGIDSKHNSYCTTHTFVKALTMGQQAAMRFIRIDTACVLSRKAARR 240
QY 241 A 241
DB 241 A 241

RESULT 7

US-09-363-573-1
Sequence 1, Application US/09363573
Patent No. 6184360

GENERAL INFORMATION:

APPLICANT: Louis B. Burton, Charles H. Schmelzer, Joanne T. Beck
TITLE OF INVENTION: Purification of NGF
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/363,573
FILING DATE:

CLASSIFICATION:
APPLICATION NUMBER: US/08/970,865
FILING DATE: 14-NO. 6184360-1997

APPLICATION NUMBER: 60/030838
FILING DATE: 11/15/1996

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/047855
FILING DATE: 5/29/1997

ATTORNEY/AGENT INFORMATION:
NAME: Torchia, PhD., Timothy E.

REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1063R2

TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:

LENGTH: 241 amino acids
 TYPE: Amino Acid
 TOPOLOGY: Linear
 US-09-363-573-1

Query Match 100.0%; Score 1270; DB 4; Length 241;
 Best Local Similarity 100.0%; Pred. No. 1.1e-142;
 Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSMLFTTLITAFILIGIOAEPHSESNVPAGHTIPQVHTKLOHSLDPLARRASAPAAAIA 60
 DB 1 MSMLFTTLITAFILIGIOAEPHSESNVPAGHTIPQVHTKLOHSLDPLARRASAPAAAIA 60
 QY 61 ARVAGOTRNTITVDPRLFKKRLRSRVLFSSTOPPREADTODLDFEVGAAPFNRTRSK 120
 DB 61 ARVAGOTRNTITVDPRLFKKRLRSRVLFSSTOPPREADTODLDFEVGAAPFNRTRSK 120
 QY 121 RSSSHPIFRHGEFSVCDVSVMVGDKTATDIDIGKEVMVLGEVINNSVFKQYFFETKCR 180
 DB 121 RSSSHPIFRHGEFSVCDVSVMVGDKTATDIDIGKEVMVLGEVINNSVFKQYFFETKCR 180
 QY 181 DPNPVDSCGIDSKMNSYCTTHTFVKALTMGKQAAFRIRIDTACVLSRAVRR 240
 DB 181 DPNPVDSCGIDSKMNSYCTTHTFVKALTMGKQAAFRIRIDTACVLSRAVRR 240
 QY 241 A 241
 DB 241 A 241

RESULT 8

US-09-447-356-3
 Sequence 3, Application US/09447356
 Patent No. 6395513

GENERAL INFORMATION:
 APPLICANT: FOSTER, KEITH ALAN
 APPLICANT: DUGAN, MICHAEL JOHN
 APPLICANT: SHONE, CLIFFORD CHARLES
 TITLE OF INVENTION: CLOSTRIDIAL TOXIN DERIVATIVES ABLE TO MODIFY PERIPHERAL
 FILE REFERENCE: 023223/0104
 CURRENT APPLICATION NUMBER: US/09/447,356
 CURRENT FILING DATE: 1999-11-22
 PRIOR APPLICATION NUMBER: 08/945,037
 PRIOR FILING DATE: 1998-01-12
 PRIOR APPLICATION NUMBER: GB 9508204.6
 PRIOR FILING DATE: 1995-04-21
 NUMBER OF SEQ ID NOS: 11
 SOFTWARE: Patentin Ver. 2.1
 SEQ ID NO 3
 LENGTH: 241
 TYPE: PRT
 ORGANISM: Murine sp.
 US-09-447-356-3

Query Match 100.0%; Score 1270; DB 4; Length 241;
 Best Local Similarity 100.0%; Pred. No. 1.1e-142;
 Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSMLFTTLITAFILIGIOAEPHSESNVPAGHTIPQVHTKLOHSLDPLARRASAPAAAIA 60
 DB 1 MSMLFTTLITAFILIGIOAEPHSESNVPAGHTIPQVHTKLOHSLDPLARRASAPAAAIA 60
 QY 61 ARVAGOTRNTITVDPRLFKKRLRSRVLFSSTOPPREADTODLDFEVGAAPFNRTRSK 120
 DB 61 ARVAGOTRNTITVDPRLFKKRLRSRVLFSSTOPPREADTODLDFEVGAAPFNRTRSK 120
 QY 121 RSSSHPIFRHGEFSVCDVSVMVGDKTATDIDIGKEVMVLGEVINNSVFKQYFFETKCR 180
 DB 121 RSSSHPIFRHGEFSVCDVSVMVGDKTATDIDIGKEVMVLGEVINNSVFKQYFFETKCR 180
 QY 181 DPNPVDSCGIDSKMNSYCTTHTFVKALTMGKQAAFRIRIDTACVLSRAVRR 240
 DB 181 DPNPVDSCGIDSKMNSYCTTHTFVKALTMGKQAAFRIRIDTACVLSRAVRR 240

DB 181 DPNPVDSCGIDSKMNSYCTTHTFVKALTMGKQAAFRIRIDTACVLSRAVRR 240
 QY 241 A 241
 DB 241 A 241

RESULT 9

PCT-US91-06950-5
 Sequence 5, Application PC/TUS9106950

GENERAL INFORMATION:
 APPLICANT: GENENTECH, INC.
 APPLICANT: ROSENTHAL, ARNON
 TITLE OF INVENTION: NOVEL NEUROTROPIC FACTOR
 NUMBER OF SEQUENCES: 100
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 460 Point San Bruno Blvd
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patin (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US91/06950
 FILING DATE: 19910924
 CLASSIFICATION: 436
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/646482
 PRIOR APPLICATION DATA:
 ATTORNEY/AGENT INFORMATION:
 NAME: Hensley, Max D.
 REGISTRATION NUMBER: 27,043
 REFERENCE/DOCKET NUMBER: 666P1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415/266-1994
 TELEFAX: 415/952-9881
 TELEFAX: 910/371-7168
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 241 amino acids
 TYPE: AMINO ACID
 TOPOLOGY: linear
 PCT-US91-06950-5

Query Match 100.0%; Score 1270; DB 5; Length 241;
 Best Local Similarity 100.0%; Pred. No. 1.1e-142;
 Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSMLFTTLITAFILIGIOAEPHSESNVPAGHTIPQVHTKLOHSLDPLARRASAPAAAIA 60
 DB 1 MSMLFTTLITAFILIGIOAEPHSESNVPAGHTIPQVHTKLOHSLDPLARRASAPAAAIA 60
 QY 61 ARVAGOTRNTITVDPRLFKKRLRSRVLFSSTOPPREADTODLDFEVGAAPFNRTRSK 120
 DB 61 ARVAGOTRNTITVDPRLFKKRLRSRVLFSSTOPPREADTODLDFEVGAAPFNRTRSK 120
 QY 121 RSSSHPIFRHGEFSVCDVSVMVGDKTATDIDIGKEVMVLGEVINNSVFKQYFFETKCR 180
 DB 121 RSSSHPIFRHGEFSVCDVSVMVGDKTATDIDIGKEVMVLGEVINNSVFKQYFFETKCR 180
 QY 181 DPNPVDSCGIDSKMNSYCTTHTFVKALTMGKQAAFRIRIDTACVLSRAVRR 240
 DB 181 DPNPVDSCGIDSKMNSYCTTHTFVKALTMGKQAAFRIRIDTACVLSRAVRR 240
 QY 241 A 241
 DB 241 A 241

RESULT 10
PCT-US95-05423-4
Sequence 4, Application PC/TUS9505423
GENERAL INFORMATION:
APPLICANT: Jack Lile
APPLICANT: Tadahiko Kohno
APPLICANT: Duane Bonam
APPLICANT: Mary S. Rosendahl
TITLE OF INVENTION: Production of Biologically Active
TITLE OF INVENTION: Recombinant Neurotrophic Protein
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSER: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05423
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/266,090
FILING DATE: 27-JUNE-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/240,122
FILING DATE: 09-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/087,912
FILING DATE: 06-JULY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/680,681
FILING DATE: 04-APRIL-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/594,126
FILING DATE: 09-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/547,750
FILING DATE: 02-JULY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/505,441
FILING DATE: 06-APRIL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: STNE200/PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 241 amino acids
TYPE: amino acid
TOPOLOGY: linear
FEATURE:
NAME/KEY: inferred amino acid sequence of human NGF
PCT-US95-05423-4
Query Match 100.0%; Score 1270; DB 5; Length 241;
Best Local Similarity 100.0%; Pred. No. 1.1e-142;
Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MSMLFTLITLTAFLIGIOAEPHSESNVPAAGHTIPQVHTKLOHSLDTRLRASAPAAIA 60
1 MSMLFTLITLTAFLIGIOAEPHSESNVPAAGHTIPQVHTKLOHSLDTRLRASAPAAIA 60

61 ARVAGQNTITVDPLFKKRLRSPRLVSTQPPREADTDLDPEVGGAAPFNRTTRSK 120
61 ARVAGQNTITVDPLFKKRLRSPRLVSTQPPREADTDLDPEVGGAAPFNRTTRSK 120
121 RSSSHPIFRGSEFVCSVSVMVGDKTATIKGEVAVLGEVNNINSVFKQYFEETCR 180
121 RSSSHPIFRGSEFVCSVSVMVGDKTATIKGEVAVLGEVNNINSVFKQYFEETCR 180
121 RSSSHPIFRGSEFVCSVSVMVGDKTATIKGEVAVLGEVNNINSVFKQYFEETCR 180
181 DPNVDSCGRGIDSKHMSYCTTHTFVKALTMGKQAMRFIRIDTACVCLSKAVR 240
181 DPNVDSCGRGIDSKHMSYCTTHTFVKALTMGKQAMRFIRIDTACVCLSKAVR 240
241 A 241
241 A 241
241 A 241

RESULT 11
US-09-675-503-1
Sequence 1, Application US/09675503
Patent No. 6423831
GENERAL INFORMATION:
APPLICANT: Burton, Louis E.
APPLICANT: Schmelzer, Charles H.
APPLICANT: Beck, Joanne T.
TITLE OF INVENTION: ISOLATION OF NEUROTROPHINS FROM A
TITLE OF INVENTION: MIXTURE CONTAINING OTHER PROTEINS AND NEUROTROPHIN VARIANTS
FILE REFERENCE: GENENT. 03702
CURRENT APPLICATION NUMBER: US/09/675,503
CURRENT FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: 60/030838
PRIOR FILING DATE: 1996-11-15
PRIOR APPLICATION NUMBER: 60/047855
PRIOR FILING DATE: 1997-05-29
PRIOR APPLICATION NUMBER: 08/970865
PRIOR FILING DATE: 1997-11-14
PRIOR APPLICATION NUMBER: 09/363573
PRIOR FILING DATE: 1999-07-29
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 242
TYPE: PRT
ORGANISM: Homo sapien
US-09-675-503-1
Query Match 100.0%; Score 1270; DB 4; Length 242;
Best Local Similarity 100.0%; Pred. No. 1.1e-142;
Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MSMLFTLITLTAFLIGIOAEPHSESNVPAAGHTIPQVHTKLOHSLDTRLRASAPAAIA 60
2 MSMLFTLITLTAFLIGIOAEPHSESNVPAAGHTIPQVHTKLOHSLDTRLRASAPAAIA 61
61 ARVAGQNTITVDPLFKKRLRSPRLVSTQPPREADTDLDPEVGGAAPFNRTTRSK 120
62 ARVAGQNTITVDPLFKKRLRSPRLVSTQPPREADTDLDPEVGGAAPFNRTTRSK 121
121 RSSSHPIFRGSEFVCSVSVMVGDKTATIKGEVAVLGEVNNINSVFKQYFEETCR 180
121 RSSSHPIFRGSEFVCSVSVMVGDKTATIKGEVAVLGEVNNINSVFKQYFEETCR 180
122 RSSSHPIFRGSEFVCSVSVMVGDKTATIKGEVAVLGEVNNINSVFKQYFEETCR 181
181 DPNVDSCGRGIDSKHMSYCTTHTFVKALTMGKQAMRFIRIDTACVCLSKAVR 240
182 DPNVDSCGRGIDSKHMSYCTTHTFVKALTMGKQAMRFIRIDTACVCLSKAVR 241
241 A 241
242 A 242

RESULT 12

US-08-910-691-11
Sequence 11, Application US/08910691
Patent No. 6015552
GENERAL INFORMATION:
APPLICANT: WATANABE, Tatsuya
APPLICANT: YOSHITOMI, Sumie
APPLICANT: SASADA, Reiko
TITLE OF INVENTION: THERAPEUTIC AGENT FOR NEUTROPENIA
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN, DIKE, BRONSTEIN, ROBERTS &
ADDRESSEE: CUSHMAN
STREET: 130 Water Street
CITY: Boston
STATE: Massachusetts
COUNTRY: US
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/910,691
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/074,969
FILING DATE: 19930604
ATTORNEY/AGENT INFORMATION:
NAME: NEUNER, George W
REGISTRATION NUMBER: 26964
REFERENCE/DOCKET NUMBER: 12345
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)523-3400
TELEFAX: (617)523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 240 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-910-691-11

Query Match 78.4%; Score 996; DB 3; Length 240;
Best Local Similarity 79.2%; Pred. No. 3.9e-110;
Matches 190; Conservative 19; Mismatches 29; Indels 2; Gaps 2;

Db 1 MSMLFYLLITFLIGIQAEPSHSNVPAGHTIPQVHWTKLOHSLDTALRRARSAPAAIA 60
1 MSMLFYLLITFLIGIQAEPSHSNVPAGHTIPQVHWTKLOHSLDTALRRARSAPAAIA 60

Qy 61 ARVAGOTRNTVDRPLFKRRLRSPRVLFSTQPREADTDODLPRVCGAAPFRTRHSK 120
61 ARVAGOTRNTVDRPLFKRRLRSPRVLFSTQPREADTDODLPRVCGAAPFRTRHSK 120

Db 61 ARVAGOTRNTVDRPLFKRRLRSPRVLFSTQPREADTDODLPRVCGAAPFRTRHSK 120
61 ARVAGOTRNTVDRPLFKRRLRSPRVLFSTQPREADTDODLPRVCGAAPFRTRHSK 120

Qy 121 RSSSHPIFRHGFSEVCDVSVMVGDKTATDIDKGEVWVLGEVNNINSVFKQYFETKCR 180
121 RSSSHPIFRHGFSEVCDVSVMVGDKTATDIDKGEVWVLGEVNNINSVFKQYFETKCR 180

Db 121 RYAEHR-SHNGEYVCCSSELMVTDKSSALIDIRHQVTVLGEIKTNSPVQYFETKCR 179
121 RYAEHR-SHNGEYVCCSSELMVTDKSSALIDIRHQVTVLGEIKTNSPVQYFETKCR 179

Qy 181 DPNPVDGCGIGIDSKHNSYCTTHTTFFKALTMQD-GKQAMRFIRIDTACVLSRKAVR 239
181 DPNPVDGCGIGIDSKHNSYCTTHTTFFKALTMQD-GKQAMRFIRIDTACVLSRKAVR 239

Db 180 EARPVKNKGCGIDDKHNSQCKTSQTYVRALTSENKLVGRWIRIDTSCVCAISRKIGR 239
180 EARPVKNKGCGIDDKHNSQCKTSQTYVRALTSENKLVGRWIRIDTSCVCAISRKIGR 239

RESULT 13
US-08-440-049-3
Sequence 3, Application US/08440049
Patent No. 5728803
GENERAL INFORMATION:
APPLICANT: Ufer, Roman
APPLICANT: Presta, Leonard G.

APPLICANT: Winslow, John W.
TITLE OF INVENTION: PANROPIC NEUTROTROPIC FACTORS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,049
FILING DATE: 12-May-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/253937
FILING DATE: 03-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P0905C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-8674
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: Amino acid
TOPOLOGY: linear
US-08-440-049-3

Query Match 51.3%; Score 651; DB 1; Length 120;
Best Local Similarity 100.0%; Pred. No. 1.3e-69;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 122 SSSHPHIFRGEFSVCDVSVMVGDKTATDIDKGEVWVLGEVNNINSVFKQYFETKCRD 181
122 SSSHPHIFRGEFSVCDVSVMVGDKTATDIDKGEVWVLGEVNNINSVFKQYFETKCRD 181

Db 1 SSSHPHIFRGEFSVCDVSVMVGDKTATDIDKGEVWVLGEVNNINSVFKQYFETKCRD 60
1 SSSHPHIFRGEFSVCDVSVMVGDKTATDIDKGEVWVLGEVNNINSVFKQYFETKCRD 60

Qy 182 PNPVDGCGIGIDSKHNSYCTTHTTFFKALTMQD-GKQAMRFIRIDTACVLSRKAVRA 241
182 PNPVDGCGIGIDSKHNSYCTTHTTFFKALTMQD-GKQAMRFIRIDTACVLSRKAVRA 241

Db 61 PNPVDGCGIGIDSKHNSYCTTHTTFFKALTMQD-GKQAMRFIRIDTACVLSRKAVRA 120
61 PNPVDGCGIGIDSKHNSYCTTHTTFFKALTMQD-GKQAMRFIRIDTACVLSRKAVRA 120

RESULT 14
US-08-441-513A-3
Sequence 3, Application US/08441513A
Patent No. 5981480
GENERAL INFORMATION:
APPLICANT: Ufer, Roman
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Panthropic Neurotrophic Factors
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/441,513A
FILING DATE: 15-May-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/253937
FILING DATE: 03-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Phd., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P0905C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-441-513A-3

Query Match 51.3%; Score 651; DB 2; Length 120;
Best Local Similarity 100.0%; Pred. No. 1.3e-69;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 122 SSSHIFHRRGEPSVCDVSVMVGDITATDIDKGEVMTLGEVNIINNSVFKQYFETKCRD 181
|||
DB 1 SSSHIFHRRGEPSVCDVSVMVGDITATDIDKGEVMTLGEVNIINNSVFKQYFETKCRD 60
|||
QY 182 PNPVDSGCRGIDSKMNSYCTTHTFVKALTMDSKQAAWRFIRIDTACVLSRKAVRRA 241
|||
DB 61 PNPVDSGCRGIDSKMNSYCTTHTFVKALTMDSKQAAWRFIRIDTACVLSRKAVRRA 120
|||

RESULT 15

US-08-581-662-31
Sequence 31, Application US/08581662
Patent No. 6121235
GENERAL INFORMATION:
APPLICANT: Gao, Wei-Qiang
TITLE OF INVENTION: Treatment of Balance Impairments
FILE REFERENCE: P0981
CURRENT APPLICATION NUMBER: US/08/581,662
CURRENT FILING DATE: 1995-12-29
NUMBER OF SEQ ID NOS: 36
SEQ ID NO 31
LENGTH: 120
TYPE: PRT
ORGANISM: Homo sapiens
US-08-581-662-31

Query Match 51.3%; Score 651; DB 3; Length 120;
Best Local Similarity 100.0%; Pred. No. 1.3e-69;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 122 SSSHIFHRRGEPSVCDVSVMVGDITATDIDKGEVMTLGEVNIINNSVFKQYFETKCRD 181
|||
DB 1 SSSHIFHRRGEPSVCDVSVMVGDITATDIDKGEVMTLGEVNIINNSVFKQYFETKCRD 60
|||
QY 182 PNPVDSGCRGIDSKMNSYCTTHTFVKALTMDSKQAAWRFIRIDTACVLSRKAVRRA 241
|||
DB 61 PNPVDSGCRGIDSKMNSYCTTHTFVKALTMDSKQAAWRFIRIDTACVLSRKAVRRA 120
|||

Search completed: June 6, 2003, 10:52:04
Job time: 13.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 6, 2003, 10:46:22 ; Search time 32.5 Seconds

(without alignments)
988.105 Million cell updates/sec

Title: US-09-788-188-1

Sequence: 1 MSMLFYLLTFLIGIOAEP.....FIRIDTACVCLSKRAVRA 241

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

```

1: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:*
2: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
3: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
4: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*
5: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:*
6: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:*
7: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:*
8: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:*
9: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:*
10: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:*
11: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:*
12: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:*
13: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:*
14: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:*
15: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:*
16: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:*
17: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1996.DAT:*
18: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:*
19: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*
20: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*
21: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1270	100.0	241	AA13063	Human NGF Smal-Apa
2	1270	100.0	241	AA13063	Human nerve growth
3	1270	100.0	241	AA13063	Human nerve growth
4	1270	100.0	241	AA13063	Human nerve growth
5	1270	100.0	241	AA13063	Human nerve growth
6	1270	100.0	241	AA13063	Human nerve growth
7	1270	100.0	241	AA13063	Human nerve growth
8	1270	100.0	241	AA13063	Human nerve growth
9	1270	100.0	241	AA13063	Human nerve growth
10	1270	100.0	241	AA13063	Human nerve growth

11	1270	100.0	241	23	AB049994
12	1270	100.0	245	5	AA040038
13	1267	99.8	307	14	AA15241
14	1266	99.7	241	22	AA067865
15	1266	99.7	307	14	AA137799
16	1264	99.5	307	19	AA069725
17	1238	97.5	239	14	AA13910
18	1188.5	93.6	241	12	AA13886
19	1175	92.5	222	21	AA090884
20	1096	86.3	240	23	AA050845
21	1096	86.3	307	5	AA040036
22	1093	86.1	307	14	AA040039
23	996	78.4	240	14	AA135240
24	996	78.4	240	14	AA135240
25	996	78.4	240	13	AA156451
26	991	78.0	240	15	AA156451
27	682	53.7	129	14	AA137539
28	682	53.7	129	14	AA137539
29	661	52.0	124	13	AA124145
30	657.5	51.8	124	13	AA124145
31	651	51.3	120	20	AA122751
32	651	51.3	120	21	AA122751
33	651	51.3	120	21	AA122751
34	651	51.3	120	22	AA122751
35	648	51.0	156	23	AA150303
36	648	51.0	156	23	AA150303
37	648	51.0	157	22	AA150303
38	648	51.0	157	22	AA150303
39	647.5	51.0	156	23	AA150301
40	647.5	51.0	157	22	AA150301
41	647	50.9	261	10	AA150301
42	647	50.9	262	7	AA150301
43	643	50.6	120	17	AA150301
44	642	50.6	118	10	AA150301
45	642	50.6	119	5	AA150301

ALIGNMENTS

RESULT 1	AA13063	Standard; Protein, 241 AA.
AC	AA13063;	
DT	30-SEP-1991	(first entry)
DE	Human NGF Smal-Apai fragment prod.	
KW	Expression vector; human nerve growth factor; yeast;	
KW	senile dementia.	
OS	Homo sapiens.	
PN	JP03139285-A.	
PD	13-JUN-1991.	
PF	20-DEC-1989;	89UP-0328199.
PR	27-JUL-1989;	89UP-0192581.
PA	(TAKE) TAKEDA CHEMICAL IND KK.	
DR	WPI, 1991-218449/30.	
DR	N-PSDB; AAQ12638.	
PT	New yeast expression vector - used in produ. of human nerve growth	
PT	factor from corresp. yeast.	
PS	Disclosure; Fig 1(1-2); 14pp; Japanese.	

Human beta nerve g
Sequence encoded b
Human pre-pro nerv
Amino acid sequenc
Human NGF. Homo 8
Human beta-nerve g
Nerve growth facto
NGF with pro-regio
Human proNGF prote
Mouse nerve growth
Sequence encoded b
Cloned mouse pre-p
Sequence of pro re
Human NGF-2/NT-3 e
NGF/NT-3 in pTb13
Recombinant beta-N
Chimeric neurotrop
Human growth facto
N-terminal of neut
Nerve growth facto
NGF-beta amino aci
Nerve growth facto
Nerve growth facto
Amino acid sequenc
Synthetic nerve gr
Nerve growth facto
Amino acid sequenc
Human nerve growth
Human beta-nerve g
Panitropic neurotro
Human nerve growth
Sequence encoded b

CC Human NGF is useful as a reagent for study of the nervous system, and
 CC for treatment of senile dementia. The DNA encoding this fragment was
 CC derived from the human gene or is synthesized chemically.
 CC See also AAQ12639.
 CC XX

SO Sequence 241 AA;

Query Match 100.0%; Score 1270; DB 12; Length 241;
 Best Local Similarity 100.0%; Pred. No. 1.3e-134;
 Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSMLFYTLITAFILGIGQAEPSHESNVPAGHTTPOVHWTLOHSLDTALRRARSAAPAAIA 60
 DB 1 MSMLFYTLITAFILGIGQAEPSHESNVPAGHTTPOVHWTLOHSLDTALRRARSAAPAAIA 60
 QY 61 ARVAGQTRNITVDPRILFKKRLRSRVLSTQPPREAADTODLDFEYGAAPFRTRRSK 120
 DB 61 ARVAGQTRNITVDPRILFKKRLRSRVLSTQPPREAADTODLDFEYGAAPFRTRRSK 120
 QY 121 RSSSHPIFRHGEFSVCDSSVWVGDKTTAIDIKGEVWVLGEVNNINSVFQYFFETKCR 180
 DB 121 RSSSHPIFRHGEFSVCDSSVWVGDKTTAIDIKGEVWVLGEVNNINSVFQYFFETKCR 180
 QY 181 DPNVDSGCGRIDSKHNSYCTTHTFVKALTMGQAAAFRIRIDTACVLSRAVRR 240
 DB 181 DPNVDSGCGRIDSKHNSYCTTHTFVKALTMGQAAAFRIRIDTACVLSRAVRR 240
 QY 241 A 241
 DB 241 A 241

RESULT 2

AA01474 standard; Protein; 241 AA.

AC AA01474;
 DT 26-APR-1991 (first entry)
 DE Human nerve growth factor.
 KW NGF; senile dementia.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Peptide 1..18
 FT Protein /label= signal sequence
 FT Protein /label= pro-NGF
 FT Protein /label= mature NGF
 FT Disulfide-bond 135..202
 FT Disulfide-bond 180..230
 FT Disulfide-bond 190..232
 PN EP41451-A.
 PD 27-FEB-1991.
 PF 17-AUG-1990; 90EP-0115815.
 PR 21-AUG-1989; 89JP-0212980.
 PR 20-DEC-1989; 89JP-0328198.
 PR 13-APR-1990; 90JP-0096252.
 PR 07-JUN-1990; 90JP-0147352.
 PA (TAKE) TAKEDA CHEMICALS IND KK.
 PI Kakimura A, Nakahama K, Yoshimura K, Kaisho Y, Iwanai M;
 XX WPL; 1991-059398/09.

DR N-PSDB; AAQ10620.

XX Human nerve growth factor containing cysteine residues - used as
 PT reagent and therapeutic drug for senile dementia.
 XX PS

PS Claim 1; Fig 1; 33pp; English.

CC The sequence was deduced from a clone isolated from a lambda EMBL3
 CC genomic library prepd. from human leukocyte DNA, using a probe
 CC synthesized based on the sequence of the known human NGF gene [A.
 CC Ulrich et al., Nature 303, 821 (1983)]. The clone, betaLN2113,
 CC isolated from the library was cleaved with SmaI and ApaI to remove
 CC a 1kb fragment contg. the gene which was then inserted into plasmid
 CC pBluescript IIK to obtain pNGFPI07G. The gene was sequenced from
 CC this plasmid using Sequase (Biochemical). The sequence of the
 CC protein coding region was found to be in complete agreement with
 CC that of Ulrich et al. The sequence was used to produce
 CC recombinant h-NGF for use in the prodn. of drugs for e.g. senile
 CC dementia.

SO Sequence 241 AA;

Query Match 100.0%; Score 1270; DB 12; Length 241;
 Best Local Similarity 100.0%; Pred. No. 1.3e-134;
 Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSMLFYTLITAFILGIGQAEPSHESNVPAGHTTPOVHWTLOHSLDTALRRARSAAPAAIA 60
 DB 1 MSMLFYTLITAFILGIGQAEPSHESNVPAGHTTPOVHWTLOHSLDTALRRARSAAPAAIA 60
 QY 61 ARVAGQTRNITVDPRILFKKRLRSRVLSTQPPREAADTODLDFEYGAAPFRTRRSK 120
 DB 61 ARVAGQTRNITVDPRILFKKRLRSRVLSTQPPREAADTODLDFEYGAAPFRTRRSK 120
 QY 121 RSSSHPIFRHGEFSVCDSSVWVGDKTTAIDIKGEVWVLGEVNNINSVFQYFFETKCR 180
 DB 121 RSSSHPIFRHGEFSVCDSSVWVGDKTTAIDIKGEVWVLGEVNNINSVFQYFFETKCR 180
 QY 181 DPNVDSGCGRIDSKHNSYCTTHTFVKALTMGQAAAFRIRIDTACVLSRAVRR 240
 DB 181 DPNVDSGCGRIDSKHNSYCTTHTFVKALTMGQAAAFRIRIDTACVLSRAVRR 240
 QY 241 A 241
 DB 241 A 241

RESULT 3

AA01858 standard; Protein; 241 AA.

AC AA01858;
 DT 21-NOV-1991 (first entry)
 DE Human nerve growth factor.
 KW hNGF.
 OS Homo sapiens.
 PN JP03175976-A.
 PD 31-UTL-1991.
 PF 12-DEC-1989; 89JP-0320483.
 PR 30-SEP-1989; 89JP-0253796.
 PR 15-DEC-1988; 88JP-0314860.
 PR 12-DEC-1989; 89JP-0320483.
 PA (TAKE) TAKEDA CHEMICAL IND KK.

DR WPI; 1991-269694/37.
 DR N-PSDB; AAQ13397.
 XX
 XX Secretory prep. of animal protein - by culturing
 PT Schizosaccharomyces pombe which retains DNA at 3'-terminal of
 PT promoter region.
 XX
 XX Disclosure; Fig 3; 12pp; Japanese.
 XX
 XX The amino acid sequence is encoded that of human nerve growth factor
 CC (NGF). It may be expressed in Schizosaccharomyces pombe using the
 CC glyceroldehyde-3-phosphate dehydrogenase (GPD) gene promoter.
 XX
 SQ Sequence 241 AA;
 Query Match 100.0%; Score 1270; DB 12; Length 241;
 Best Local Similarity 100.0%; Pred. No. 1.3e-134;
 Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSMLFTLITLFLIGIOAEPHSESNVPAGHTIPQVHWTLOHSLDTALRRASAPAAIA 60
 DB 1 MSMLFTLITLFLIGIOAEPHSESNVPAGHTIPQVHWTLOHSLDTALRRASAPAAIA 60
 QY 61 ARVAGQRTNITVDPRLFKKRLRSRVLFTSTOPPREADTDODLDFEVGGAAPFRTRSK 120
 DB 61 ARVAGQRTNITVDPRLFKKRLRSRVLFTSTOPPREADTDODLDFEVGGAAPFRTRSK 120
 QY 121 RSSSHPIFRHGEFSVCDVSVMWGDKTTATDIDIKGEVMVLGEVINNSVFKQYFFETKCR 180
 DB 121 RSSSHPIFRHGEFSVCDVSVMWGDKTTATDIDIKGEVMVLGEVINNSVFKQYFFETKCR 180
 QY 181 DPNVDGSGCRGIDSKHNSYCTTHTFVKALTMGKQAMRFIRIDTACVCVLSKAVRR 240
 DB 181 DPNVDGSGCRGIDSKHNSYCTTHTFVKALTMGKQAMRFIRIDTACVCVLSKAVRR 240
 QY 241 A 241
 DB 241 A 241
 RESULT 4
 AAR77419
 ID AAR77419 standard; Protein; 241 AA.
 AC AAR77419;
 XX
 XX 10-FEB-1996 (first entry)
 DT
 XX Human nerve growth factor.
 DE
 XX Nerve growth factor; neurotrophic factor; therapeutic;
 KW protein refolding; NGF.
 XX
 XX Homo sapiens.
 OS
 XX
 FH Key Location/Qualifiers
 FT Protein 122..241
 FT /note= "mature protein"
 FT Region 1..121
 FT /note= "pre-region"
 XX
 XX MO9530686-A1.
 PN
 XX 16-NOV-1995.
 PD
 XX
 XX 02-MAY-1995; 95MO-US05423.
 PF
 XX 27-JUN-1994; 94US-0266080.
 PR
 XX 09-MAY-1994; 94US-0240122.
 PA (SYNT) SYNTAX-SYNERGEN NEUROSCIENCE JOINT VENTU.
 XX
 XX Bonam D, Kohno T, Lile J, Rosendahl MS;

XX
 DR WPI; 1995-404080/51.
 DR N-PSDB; AAT05437.
 XX
 XX Process for bacterial expression of recombinant neurotrophic factor
 PT - useful for promoting the survival and maintaining phenotypic
 PT differentiation of nerve and glial cells.
 XX
 XX Disclosure; Page 33-34; 57pp; English.
 XX
 XX The nerve growth factor (NGF) gene is expressed in Escherichia
 CC coli cells. The recombinant protein is solubilized and
 CC sulfonlated and allowed to refold in the presence of ppg and urea.
 CC Biologically active NGF, used for promoting the survival of and
 CC maintaining the phenotypic differentiation of nerve and glial cells,
 CC is isolated and purified. This method breaks incorrectly formed
 CC disulphide bonds and allows refolding of the factor into the correct
 CC tertiary structure required for maximum yield of full active protein.
 XX
 SQ Sequence 241 AA;
 Query Match 100.0%; Score 1270; DB 16; Length 241;
 Best Local Similarity 100.0%; Pred. No. 1.3e-134;
 Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSMLFTLITLFLIGIOAEPHSESNVPAGHTIPQVHWTLOHSLDTALRRASAPAAIA 60
 DB 1 MSMLFTLITLFLIGIOAEPHSESNVPAGHTIPQVHWTLOHSLDTALRRASAPAAIA 60
 QY 61 ARVAGQRTNITVDPRLFKKRLRSRVLFTSTOPPREADTDODLDFEVGGAAPFRTRSK 120
 DB 61 ARVAGQRTNITVDPRLFKKRLRSRVLFTSTOPPREADTDODLDFEVGGAAPFRTRSK 120
 QY 121 RSSSHPIFRHGEFSVCDVSVMWGDKTTATDIDIKGEVMVLGEVINNSVFKQYFFETKCR 180
 DB 121 RSSSHPIFRHGEFSVCDVSVMWGDKTTATDIDIKGEVMVLGEVINNSVFKQYFFETKCR 180
 QY 181 DPNVDGSGCRGIDSKHNSYCTTHTFVKALTMGKQAMRFIRIDTACVCVLSKAVRR 240
 DB 181 DPNVDGSGCRGIDSKHNSYCTTHTFVKALTMGKQAMRFIRIDTACVCVLSKAVRR 240
 QY 241 A 241
 DB 241 A 241
 RESULT 5
 AAR66688
 ID AAR66688 standard; Protein; 241 AA.
 AC AAR66688;
 XX
 XX 23-AUG-1995 (first entry)
 DT
 XX Human nerve growth factor.
 DE
 XX Human nerve growth factor; hNGF; polyclonal antibody;
 KW immunogen; enzyme immunoassay.
 XX
 XX Homo sapiens.
 OS
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..18
 FT /label= sig_peptide
 FT Peptide 19..121
 FT /label= pro_peptide
 FT Misc-difference 8
 FT /note= "corresponding codon TCG"
 FT Misc-difference 59
 FT /note= "corresponding codon TAT"
 FT Misc-difference 173
 FT /note= "corresponding codon TAG"
 FT Disulfide-bond 136..201

FT Disulfide-bond 179..229
 FT Disulfide-bond 189..231
 XX JP06317587-A.
 XX
 PD 15-NOV-1994.
 XX
 PF 14-FEB-1991; 91JP-0021181.
 XX
 PR 31-AUG-1990; 90JP-0231317.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 DR WPI; 1995-033116/05.
 DR N-PSJB; AA079871.
 XX
 PT Polyclonal antibody against human nerve growth factor (NGF) -
 PT useful to detect human NGF, for diagnosis of disease
 XX
 PS Example 1; Pages 31-33; 35pp; Japanese.
 XX
 CC AA079871 encodes AAR6668 human nerve growth factor (NGF), the
 CC protein was used as an immunogen to generate a polyclonal
 CC antibody against hNGF. The polyclonal antibody can be used
 CC to detect and determine hNGF pref. by enzyme immunoassay.
 CC
 SQ Sequence 241 AA;
 Query Match 100.0%; Score 1270; DB 16; Length 241;
 Best Local Similarity 100.0%; Pred. No. 1.3e-134;
 Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSMLFYTLITAFILGIGQAEPHSESNVPAGHTIPQVHWTKLOHSIDTLARRASAPAAIA 60
 DB 1 MSMLFYTLITAFILGIGQAEPHSESNVPAGHTIPQVHWTKLOHSIDTLARRASAPAAIA 60
 QY 61 ARVAGQTRNITVDPRLPFKKRLSPRVLPSTQPREAADTODLDFEVGAAPFNRTHSK 120
 DB 61 ARVAGQTRNITVDPRLPFKKRLSPRVLPSTQPREAADTODLDFEVGAAPFNRTHSK 120
 QY 121 RSSSHPIFRHGEFSVCDVSVMGDKTTATDINGKKEVMVLGEVINNSVFKQYFFETKCR 180
 DB 121 RSSSHPIFRHGEFSVCDVSVMGDKTTATDINGKKEVMVLGEVINNSVFKQYFFETKCR 180
 QY 181 DPNPVDSCGCGIDSKMNSYCTTHTFVKALITMDGKQAAWRFIRIDTACVCVLSRKAVRR 240
 DB 181 DPNPVDSCGCGIDSKMNSYCTTHTFVKALITMDGKQAAWRFIRIDTACVCVLSRKAVRR 240
 QY 241 A 241
 DB 241 A 241
 RESULT 6
 AAW26237
 ID AAW26237 standard; Protein; 241 AA.
 XX
 AC AAW26237;
 XX
 DT 16-MAR-1998 (first entry)
 XX
 DE Human preproNGF.
 XX
 KW Fusion protein; hydrophilic spacer; recombinant; expression system;
 KW carboxypeptidase; preproNGF.
 XX
 OS Homo sapiens.
 XX
 PN WO9728272-A1.
 XX
 PD 07-AUG-1997.
 XX
 PP 31-JAN-1997; 97WO-US01470.

XX
 PR 31-JAN-1996; 96US-0595043.
 XX
 PA (TECH-) TECHNOLOGENE INC.
 XX
 PI Sgarlato GD;
 XX
 DR WPI; 1997-402624/37.
 DR N-PSDB; AAT80162.
 XX
 PT Recombinant protein expression system for fusion protein production
 PT - useful for high quantity production of authentic recombinant
 PT proteins
 XX
 PS Example 6; Page 140-141; 194pp; English.
 XX
 CC A novel recombinant vector has been developed which comprises a
 CC nucleotide sequence encoding a fusion protein. The fusion protein
 CC comprises three domains joined together in order, from N-terminus to
 CC C-terminus, of a first domain comprising a protein of interest, a second
 CC domain comprising a hydrophilic spacer and an affinity domain, each
 CC human preproNGF, used in example 6 of the present invention. The
 CC recombinant vector is used for the production of authentic recombinant
 CC proteins of interest. The method of the invention is useful for the
 CC expression of fusion proteins capable of isolation by affinity
 CC chromatography in pro- or eukaryotic cells. This method allows
 CC for the efficient cleavage and generation of authentic proteins of
 CC interest that do not contain extraneous (i.e. non-naturally occurring)
 CC amino acids.
 SQ Sequence 241 AA;
 Query Match 100.0%; Score 1270; DB 18; Length 241;
 Best Local Similarity 100.0%; Pred. No. 1.3e-134;
 Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSMLFYTLITAFILGIGQAEPHSESNVPAGHTIPQVHWTKLOHSIDTLARRASAPAAIA 60
 DB 1 MSMLFYTLITAFILGIGQAEPHSESNVPAGHTIPQVHWTKLOHSIDTLARRASAPAAIA 60
 QY 61 ARVAGQTRNITVDPRLPFKKRLSPRVLPSTQPREAADTODLDFEVGAAPFNRTHSK 120
 DB 61 ARVAGQTRNITVDPRLPFKKRLSPRVLPSTQPREAADTODLDFEVGAAPFNRTHSK 120
 QY 121 RSSSHPIFRHGEFSVCDVSVMGDKTTATDINGKKEVMVLGEVINNSVFKQYFFETKCR 180
 DB 121 RSSSHPIFRHGEFSVCDVSVMGDKTTATDINGKKEVMVLGEVINNSVFKQYFFETKCR 180
 QY 181 DPNPVDSCGCGIDSKMNSYCTTHTFVKALITMDGKQAAWRFIRIDTACVCVLSRKAVRR 240
 DB 181 DPNPVDSCGCGIDSKMNSYCTTHTFVKALITMDGKQAAWRFIRIDTACVCVLSRKAVRR 240
 QY 241 A 241
 DB 241 A 241
 RESULT 7
 AAW48886
 ID AAW48886 standard; Protein; 241 AA.
 XX
 AC AAW48886;
 XX
 DT 12-OCT-1998 (first entry)
 XX
 DE Human prepro-nerve growth factor beta chain.
 XX
 KW Neurotrophin; nerve growth factor; NGF; human; purification;
 KW hydrophobic interaction chromatography.
 XX
 OS Homo sapiens.

```

FH Key Location/Qualifiers
FT Protein 1..121
FT /label= Prepro_region
FT Protein 122..241
FT /label= Mat_protein
FT Modified-site 167
FT /note= "N-glycosylated"
FT Region 179..189
FT /note= "conserved Cys-containing region involved in
FT Cys knot motif"
FT Region 229..231
FT /note= "conserved Cys-containing region involved in
FT Cys knot motif"
XX MO9821234-A2.
XX 22-MAY-1998.
XX 14-NOV-1997; 97MO-US21068.
XX 29-MAY-1997; 97US-0047855.
XX 15-NOV-1996; 96US-0030838.
XX (GRTX ) GENENTECH INC.
XX Beck JT, Burton LE, Schmelzer CH;
XX WPI; 1998-32233/28.
XX
XX Isolation of neurotrophin(s) from, e.g. mls-folded or glycosylated
XX variant(s) - using hydrophobic interaction chromatography,
XX optionally in combination with high performance cation exchange
XX chromatography
XX
XX Disclosure; Fig 4; 59pp; English.
XX
XX This polypeptide comprises the human nerve growth factor (NGF)
XX beta chain precursor. Methods are provided for large-scale
XX purification of neurotrophins, including mature NGF, suitable for
XX clinical use. A claimed method comprises: (1) separating the
XX neurotrophin from the other proteins using a hydrophobic
XX interaction chromatography resin (HICR); and optionally (2)
XX separating the neurotrophin from a chemical variant by high
XX performance cation exchange chromatography (HPEC). The processes
XX can also be used for purification of e.g. mouse NGF (see AAM48887),
XX brain-derived neurotrophic factor (see AAM48888), neurotrophin-4/5,
XX (see AAM48890) and neurotrophin-3 (see AAM48889). The processes allow
XX separation of neurotrophins from various undesirable misprocessed,
XX misfolded, size, glycosylated or charge forms. They allow selective
XX separation from their variants and other molecules, and from other
XX polypeptides with high pi. The processes are applicable to
XX starting materials from various sources, including fermentation
XX broths or lysed bacterial or mammalian cells.
XX
XX Sequence 241 AA;
SQ
Query Match 100.0%; Score 1270; DB 19; Length 241;
Best Local Similarity 100.0%; Pred. No. 1.3e-134;
Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSMLFTLLTAFLIGIOAEPHSSNVPAGHTIPQVHTKLOHSLDRLRRASAPAAIA 60
DB 1 MSMLFTLLTAFLIGIOAEPHSSNVPAGHTIPQVHTKLOHSLDRLRRASAPAAIA 60
QY 61 ARVAGOTRNTVDPRLFKKRLRSPVLPSTOPPREAADTODLDFEVGAAPFNRTTRSK 120
DB 61 ARVAGOTRNTVDPRLFKKRLRSPVLPSTOPPREAADTODLDFEVGAAPFNRTTRSK 120
QY 121 RSSSHPIFRHGEFVCDVSVMVGDKTTADIKGKVMVLGEVINNSVFKOYFEETKCR 180
DB 121 RSSSHPIFRHGEFVCDVSVMVGDKTTADIKGKVMVLGEVINNSVFKOYFEETKCR 180
QY 181 DPNPVDSCGCGIDSKMNSYCTTHTFVKALTMGQKQAMRFIRIDPACVLSRKAVER 240

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DB 181 DPNPVDSCGCGIDSKMNSYCTTHTFVKALTMGQKQAMRFIRIDPACVLSRKAVER 240
QY 241 A 241
DB 241 A 241
RESULT 8
AA07303
ID AA07303 standard; Protein; 241 AA.
XX
XX AA07303;
XX
XX 06-JUL-1999 (first entry)
XX
XX Human nerve growth factor beta protein.
XX
XX Cerebrospinal; axon; growth; mammal; spinal cord injury; lesion; NGF2;
XX expression vector; neurotrophin; nerve growth factor 2; neurotrophin 3;
XX NT3; voluntary motor function.
XX
XX Homo sapiens.
XX
XX MO9900148-A2.
XX
XX 07-JAN-1999.
XX
XX 30-JUN-1998; 98MO-US13778.
XX
XX 30-JUN-1997; 97US-0051255.
XX
XX (REGC ) UNIV CALIFORNIA.
XX
XX Gage FH, Grill R, Tuszynski MH;
XX WPI; 1999-095478/08.
XX
XX N-PSDB; AAX34366.
XX
XX Treating spinal cord injuries in a mammal - by inducing growth of
XX cerebrospinal projection axons using a recombinant vector for
XX expressing CST neurotrophin
XX
XX Disclosure; Fig 6; 49pp; English.
XX
XX The invention relates to a method of inducing cerebrospinal projection
XX (CST) axon growth in a mammal with a spinal cord injury that involves
XX a CST lesion by delivering a recombinant expression vector for CST
XX neurotrophin, such as this sequence - nerve growth factor beta. The
XX method is used to induce partial recovery of voluntary motor function
XX in a mammal after disruption of corticospinal projections in the spinal
XX cord.
XX
XX Sequence 241 AA;
SQ
Query Match 100.0%; Score 1270; DB 20; Length 241;
Best Local Similarity 100.0%; Pred. No. 1.3e-134;
Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSMLFTLLTAFLIGIOAEPHSSNVPAGHTIPQVHTKLOHSLDRLRRASAPAAIA 60
DB 1 MSMLFTLLTAFLIGIOAEPHSSNVPAGHTIPQVHTKLOHSLDRLRRASAPAAIA 60
QY 61 ARVAGOTRNTVDPRLFKKRLRSPVLPSTOPPREAADTODLDFEVGAAPFNRTTRSK 120
DB 61 ARVAGOTRNTVDPRLFKKRLRSPVLPSTOPPREAADTODLDFEVGAAPFNRTTRSK 120
QY 121 RSSSHPIFRHGEFVCDVSVMVGDKTTADIKGKVMVLGEVINNSVFKOYFEETKCR 180
DB 121 RSSSHPIFRHGEFVCDVSVMVGDKTTADIKGKVMVLGEVINNSVFKOYFEETKCR 180
QY 181 DPNPVDSCGCGIDSKMNSYCTTHTFVKALTMGQKQAMRFIRIDPACVLSRKAVER 240

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Db 181 DENPVDGCGRIDSKHNSYCTTHTFVKALTMDSKQAMRFIRIDTACVLSRKAVER 240
 QY 241 A 241
 Db 241 A 241

RESULT 9
 AAB66929
 ID AAB66929 standard; Protein; 241 AA.

AC AAB66929;
 DT 17-APR-2001 (first entry)
 XX
 DE Human NGF.
 XX
 KM Human; neuroprotective; neuronal factor; NF; neurotrophin-3; NT-3;
 KW neurodegenerative disease; Alzheimer's disease; Parkinson's disease;
 KM Huntington's chorea; nerve damage; nerve growth factor; NGF.
 XX
 OS Homo sapiens.
 XX
 FN US6174701-B1.
 XX
 PD 16-JAN-2001.
 XX
 PF 31-MAY-1995; 95US-0455741.
 XX
 PR 15-MAR-1990; 90US-0494024.
 PR 31-JAN-1995; 95US-0381030.
 PR 12-DEC-1989; 89US-0449811.
 XX
 PA (GERTH) GENENTECH INC.
 XX
 PI Rosenthal A, Winslow JW;
 XX
 DR WPI; 2001-201803/20.
 XX
 PT New nucleic acid encoding a neuronal factor (rat precursor
 PT neurotrophin-3; NT-3), useful in the recombinant preparation of NT-3,
 PT which is useful for enhancing the survival of nerve cells and treating
 PT neurodegenerative diseases -
 XX
 PS Disclosure; Fig 3; 18pp; English.
 XX
 CC The present invention relates to neuronal factor (NF) also known as
 CC neurotrophin-3/NT-3; see AAF55829-AAF5830 and AAB66927-AAB66928). NF
 CC is useful in treating neurodegenerative diseases, e.g. Alzheimer's
 CC disease, Parkinson's disease, Huntington's chorea and other conditions
 CC characterised by necrosis or loss of neurons. NF is also useful for
 CC treating damaged nerves, e.g. nerves damaged by traumatic conditions such
 CC as burns or wounds. The present sequence is human nerve growth factor
 CC (NGF), which was used in a sequence homology alignment with human NF
 CC protein.
 XX
 SQ Sequence 241 AA;

Query Match 100.0%; Score 1270; DB 22; Length 241;
 Best Local Similarity 100.0%; Pred. No. 1.3e-134;
 Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSMLFYTLTAFLIGIOAEPHSESNVPAHTTPOVWMTKQHSIDTLRLRARSAPAAIA 60
 Db 1 MSMLFYTLTAFLIGIOAEPHSESNVPAHTTPOVWMTKQHSIDTLRLRARSAPAAIA 60
 QY 61 ARVAGGTNRITVDPRLFKKRLRSPRVLFSTOPPREAATODLDFEVGAAPFNRTRSK 120
 Db 61 ARVAGGTNRITVDPRLFKKRLRSPRVLFSTOPPREAATODLDFEVGAAPFNRTRSK 120
 QY 121 RSSSHPIFHHGSEVCDVSVMWGDKTTATDIDKGEVMTLGEVNNINSVEKQYFFETKCR 180
 Db 121 RSSSHPIFHHGSEVCDVSVMWGDKTTATDIDKGEVMTLGEVNNINSVEKQYFFETKCR 180
 QY 121 RSSSHPIFHHGSEVCDVSVMWGDKTTATDIDKGEVMTLGEVNNINSVEKQYFFETKCR 180
 Db 121 RSSSHPIFHHGSEVCDVSVMWGDKTTATDIDKGEVMTLGEVNNINSVEKQYFFETKCR 180

QY 181 DENPVDGCGRIDSKHNSYCTTHTFVKALTMDSKQAMRFIRIDTACVLSRKAVER 240
 Db 181 DENPVDGCGRIDSKHNSYCTTHTFVKALTMDSKQAMRFIRIDTACVLSRKAVER 240
 QY 241 A 241
 Db 241 A 241

RESULT 10
 AAE18904
 ID AAE18904 standard; Protein; 241 AA.

AC AAE18904;
 DT 21-MAY-2002 (first entry)
 XX
 DE Human beta nerve growth factor (NGF) protein.
 XX
 KM Human; nerve growth factor; NGF; neurotrophin; cholinergic neuron;
 KW gene therapy; neuroprotective; Alzheimer's disease; Parkinson's disease;
 KM neurodegenerative condition; ALS; amyotrophic lateral sclerosis.
 XX
 OS Homo sapiens.
 XX
 FN W020020774-A2.
 XX
 PD 31-JAN-2002.
 XX
 PF 17-MAY-2001; 2001WO-US16122.
 XX
 PR 19-JUL-2000; 2000US-0620174.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Tuszyński MH;
 XX
 DR WPI; 2002-195846/25.
 DR N-PSDB; AAD30144.
 XX
 PT Delivering therapeutic neurotrophin to targeted defective, diseased or
 PT damaged cholinergic neurons, useful for treating neurodegenerative
 PT disease, comprises administering a neurotrophin encoding transgene into
 PT the brain -
 XX
 PS Example 1; Fig 2; 38pp; English.
 XX
 CC The invention relates to a method for delivering therapeutic neurotrophin
 CC to targeted defective, diseased or damaged cholinergic neurons in
 CC the mammalian brain. The method comprises delivering a neurotrophic
 CC composition comprising a neurotrophin encoding transgene into one or more
 CC delivery sites within a region of the brain containing targeted neurons.
 CC The method is useful for treating neurodegenerative conditions such as
 CC Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis
 CC (ALS) in primates by stimulating the growth of neurons thus recovering
 CC neurological function. The present sequence is human nerve growth factor
 CC (NGF-2) protein which is a neurotrophin.
 XX
 SQ Sequence 241 AA;

Query Match 100.0%; Score 1270; DB 23; Length 241;
 Best Local Similarity 100.0%; Pred. No. 1.3e-134;
 Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSMLFYTLTAFLIGIOAEPHSESNVPAHTTPOVWMTKQHSIDTLRLRARSAPAAIA 60
 Db 1 MSMLFYTLTAFLIGIOAEPHSESNVPAHTTPOVWMTKQHSIDTLRLRARSAPAAIA 60
 QY 61 ARVAGGTNRITVDPRLFKKRLRSPRVLFSTOPPREAATODLDFEVGAAPFNRTRSK 120
 Db 61 ARVAGGTNRITVDPRLFKKRLRSPRVLFSTOPPREAATODLDFEVGAAPFNRTRSK 120

QY 121 RSSHPHFRRGFSVCDSSVWVGDKTTATDICKKEVWVLGEVININNSVFKQYFFETKCR 180
 DB 121 RSSHPHFRRGFSVCDSSVWVGDKTTATDICKKEVWVLGEVININNSVFKQYFFETKCR 180
 QY 181 DPNPVDSCGRGIDSKHMNSYCTTHTTFVKALTMGKQAMRFIRIDTACVCLSRKAVR 240
 DB 181 DPNPVDSCGRGIDSKHMNSYCTTHTTFVKALTMGKQAMRFIRIDTACVCLSRKAVR 240
 QY 241 A 241
 DB 241 A 241
 RESULT 11
 ID ABB04994 standard; Protein; 241 AA.
 AC ABB04994;
 DT 19-MAR-2002 (first entry)
 DE Human beta nerve growth factor protein.
 KW Human: nerve growth factor 2; beta nerve growth factor; NGF-2; NT-3;
 KW neurotrophin-3; nervous system growth factor; neuronal atrophy;
 KW aging; brain; axonal growth; neuron; neurotrophic; neuroprotective;
 KW anti-aging; cholinergic neuron growth stimulator; gene therapy.
 OS Homo sapiens.
 PN US2001043920-A1.
 PD 22-NOV-2001.
 PF 05-DEC-2000; 2000US-0730790.
 PR 15-APR-1998; 98US-0060543.
 PA (TUSZ/) TUSZYNSKI M H.
 PA (BLES/) BLESCH A.
 PI Tuszynski MH, Blesch A;
 DR WPI; 2002-105567/14.
 DR N-PSDB; ABA92503.
 PT Ameliorating neuronal atrophy and loss of accompanying normal aging
 PT comprises delivering a transgene encoding a growth factor to a
 PT mammalian brain to stimulate axon growth in cholinergic neurons -
 PS Disclosure; Fig 6 1-2; 18pp; English.
 XX The present invention describes a method for ameliorating neuronal
 CC atrophy and loss of accompanying normal aging in the mammalian brain.
 CC The method comprises delivering a growth factor (GF)-encoding transgene
 CC to preselected delivery sites in the brain, so that the encoded GF is
 CC expressed in the brain and stimulates axonal growth in targeted
 CC GF-receptive neurons. The growth factor has neurotrophic, neuroprotective
 CC and anti-aging activities, and can be used as a cholinergic neuron
 CC growth stimulator and in gene therapy. The method is used to
 CC ameliorating neuronal atrophy and loss of accompanying normal aging, in
 CC the human brain. The present sequence represents human beta nerve growth
 CC factor, which is given in the exemplification of the present invention.
 SO Sequence 241 AA;
 Query Match 100.0%; Score 1270; DB 23; Length 241;
 Best Local Similarity 100.0%; Pred. No. 1.3e-134;
 Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSMLFTLLTAPLIGIOAEPHSESNNVPAAGHTIPQVWMTKLOHSLDTPALRRARSAAPAAIA 60
 DB 1 MSMLFTLLTAPLIGIOAEPHSESNNVPAAGHTIPQVWMTKLOHSLDTPALRRARSAAPAAIA 60

QY 61 ARVAGQNTITVDPRLFKKRRLSPRVLFSTQPPREAADTODLDEVGGAAPFNTRRSK 120
 DB 61 ARVAGQNTITVDPRLFKKRRLSPRVLFSTQPPREAADTODLDEVGGAAPFNTRRSK 120
 QY 121 RSSHPHFRRGFSVCDSSVWVGDKTTATDICKKEVWVLGEVININNSVFKQYFFETKCR 180
 DB 121 RSSHPHFRRGFSVCDSSVWVGDKTTATDICKKEVWVLGEVININNSVFKQYFFETKCR 180
 QY 241 A 241
 DB 241 A 241
 RESULT 12
 ID AAP40038 standard; Protein; 245 AA.
 AC AAP40038;
 DT 25-JAN-1992 (first entry)
 DE Sequence encoded by portion of human beta-nerve growth factor
 DE (NGF) chromosomal gene which includes an exon.
 KW Nerve damage; therapy.
 OS Homo sapiens.
 PN EP121338-A.
 PD 10-OCT-1984.
 PF 02-MAR-1984; 84EP-0301377.
 PR 03-MAR-1983; 83US-0471962.
 PA (GETH) GENENTECH INC.
 PI Gray AM, Ullrich A;
 DR WPI; 1984-251909/41.
 DR N-PSDB; AAN40033.
 PT Human beta-nerve growth factor free from other proteins - obtd.
 PT by recombinant DNA techniques for treating nerve damage
 PS Example; Fig 5; 42pp; English.
 XX The inventors claim human beta-nerve growth factor (NGF) free from
 CC other proteins of human origin. Also claimed are the DNA sequence
 CC encoding human beta-NGF operably linked with a DNA sequence capable
 CC of effecting its expression in a recombinant host cell; a replicable
 CC expression vector contg. the DNA; and host cells transformed with
 CC the vector. The plasmid claimed is plasmid ph-beta-NGF trip 1. Using
 CC extrn. of natural materials, see e.g. EP-2139.
 SO Sequence 245 AA;
 Query Match 100.0%; Score 1270; DB 5; Length 245;
 Best Local Similarity 100.0%; Pred. No. 1.3e-134;
 Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSMLFTLLTAPLIGIOAEPHSESNNVPAAGHTIPQVWMTKLOHSLDTPALRRARSAAPAAIA 60
 DB 5 MSMLFTLLTAPLIGIOAEPHSESNNVPAAGHTIPQVWMTKLOHSLDTPALRRARSAAPAAIA 64
 QY 61 ARVAGQNTITVDPRLFKKRRLSPRVLFSTQPPREAADTODLDEVGGAAPFNTRRSK 120

Db 65 ARVAGQTRNITVDPRFLFKKRLRSRVLFTSTQPREADVDLDFEVGAAPFNRTKRSK 124
 QY 121 RSSSHPIFRHGEFSVCDVSVMWGDKTTATDIDKGEVWVLGEVINNSVFKQYFFETKCR 180
 Db 125 RSSSHPIFRHGEFSVCDVSVMWGDKTTATDIDKGEVWVLGEVINNSVFKQYFFETKCR 184
 QY 181 DPNPVDSGCRGIDSKHNSYCTTHTFVKALTMGKQAAWFRIRIDTACVCLSRKAVR 240
 Db 185 DPNPVDSGCRGIDSKHNSYCTTHTFVKALTMGKQAAWFRIRIDTACVCLSRKAVR 244
 QY 241 A 241
 Db 245 A 245

RESULT 13 AAR45241

ID AAR45241 standard; Protein; 307 AA.

AC AAR45241;
 XX 20-JUN-1994 (first entry)
 DT 20-JUN-1994 (first entry)
 DB Human pre-pro nerve growth factor.
 XX Mature; beta-nerve growth factor; pre-pro portion;
 KW expression; NGF; hNGF; treatment; Alzheimer's Disease.
 XX Homo sapiens.
 OS Homo sapiens.
 XX Key Location/Qualifiers
 FH Peptide 1..187
 FT Peptide /note= "signal peptide"
 FT Peptide 188..307
 FT Peptide /note= "mature peptide"

US5272063-A.

21-DEC-1993.

20-JUN-1989; 89US-0383118.

22-NOV-1988; 88US-0274878.
 PR 20-JUN-1989; 89US-0383118.

(SYNT) SYNTEX USA INC.

PI Baecker PA, Barnett JM, Bursztyl-Petegrew H, Chan HM, Nguyen BT,
 PI Ward C;

XX WPI; 1993-413401/51.

DR N-PSDB; AAO54283.

PT Prodn. of active mature human beta-nerve growth factor in insect
 PT cells - using baculovirus expression system, and potential use of
 PT recombinant hNGF in treatment of Alzheimer's disease
 XX Disclosure; Fig 1; 23pp; English.

CC The sequence is that of human pre-pro nerve growth factor
 CC which was used in a method of producing biologically active
 CC mature human beta-nerve growth factor in insect cells.

XX Sequence 307 AA;

Query Match 99.8%; Score 1267; DB 14; Length 307;
 Best Local Similarity 99.6%; Pred. NO. 4e-134;
 Matches 240; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSMLFTLTITAPLIGIOAEPSHSNVPAGHTIPOVHMTKLOHSLDTRLRARAPAAIA 60
 Db 67 MSMLFTLTITAPLIGIOAEPSHSNVPAGHTIPOVHMTKLOHSLDTRLRARAPAAIA 126

QY 61 ARVAGQTRNITVDPRFLFKKRLRSRVLFTSTQPREADVDLDFEVGAAPFNRTKRSK 120
 Db 127 ARVAGQTRNITVDPRFLFKKRLRSRVLFTSTQPREADVDLDFEVGAAPFNRTKRSK 186
 QY 121 RSSSHPIFRHGEFSVCDVSVMWGDKTTATDIDKGEVWVLGEVINNSVFKQYFFETKCR 180
 Db 187 RSSSHPIFRHGEFSVCDVSVMWGDKTTATDIDKGEVWVLGEVINNSVFKQYFFETKCR 246
 QY 181 DPNPVDSGCRGIDSKHNSYCTTHTFVKALTMGKQAAWFRIRIDTACVCLSRKAVR 240
 Db 247 DPNPVDSGCRGIDSKHNSYCTTHTFVKALTMGKQAAWFRIRIDTACVCLSRKAVR 306
 QY 241 A 241
 Db 307 A 307

RESULT 14 AAB67865

ID AAB67865 standard; Protein; 241 AA.

AC AAB67865;
 XX 29-JUN-2001 (first entry)
 DT 29-JUN-2001 (first entry)

DE Amino acid sequence of a human polypeptide designated PTMA-8.

KW PTMA; immune deficiency; infection; autoimmune disorder; wound closure;
 KW connective tissue disease; multiple sclerosis; rheumatoid arthritis;
 KW systemic lupus erythematosus; autoimmune pulmonary inflammation; ulcer;
 KW Guillain-Barre syndrome; autoimmune thyroiditis; myasthenia gravis;
 KW insulin dependent diabetes mellitus; graft-versus-host disease;
 KW autoimmune inflammatory eye disease; gut protection; gut regeneration;
 KW fibrosis; reperfusion injury; systemic cytokine damage.

XX Homo sapiens.

PN WO200123572-A2.

PD 05-APR-2001.

XX 29-SEP-2000; 2000WO-US41035.

PR 30-SEP-1999; 99US-0156745.
 PR 06-OCT-1999; 99US-0158942.
 PR 13-OCT-1999; 99US-0159248.
 PR 06-DEC-1999; 99US-0169344.
 PR 29-JUN-2000; 2000US-0215048.

XX (CURA-) CURAGEN CORP.

XX Prayaga SK, Vernet C, Shinkets RA, Burgess C, Spytek KA;

XX WPI; 2001-273512/28.

DR N-PSDB; AAF80462.

PT Novel polypeptides termed PTMA, and nucleic acids encoding PTMA,
 PT useful for detecting and treating diseases caused immune deficiencies -
 XX Claim 1; Page 20-22; 128pp; English.

CC The present sequence represents a PTMA-8 (not defined) polypeptide. The
 CC sequence is derived from clone AL049825. The polypeptide is 26958.5
 CC daltons. PTMA polynucleotides and polypeptides are used in the
 CC manufacture of a medicament for treating a syndrome associated with a
 CC human disease, the disease selected from a pathology associated with a
 CC PTMA. They may be useful in the treatment of various immune deficiencies
 CC and disorders. These immune deficiencies may be genetic or caused by
 CC viral as well as bacterial or fungal infections or may result from
 CC autoimmune disorders. Autoimmune disorders which may be treated using
 CC PTMA include, for example, connective tissue disease, multiple sclerosis,
 CC systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary

CC inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin
 CC dependent diabetes mellitus, myasthenia gravis, graft-versus-host disease
 CC and autoimmune inflammatory eye disease. Additionally PTMA may also be
 CC useful to promote better or faster closure of non-healing wounds,
 CC including pressure ulcers, ulcers associated with vascular insufficiency,
 CC surgical and traumatic wounds. Furthermore, PTMA may also be useful for
 CC gut protection or regeneration and treatment of lung or liver fibrosis,
 CC reperfusion injury in various tissue, and conditions resulting from
 CC systemic cytokine damage.

XX Sequence 241 AA;

Query Match 99.7%; Score 1266; DB 22; Length 241;
 Best Local Similarity 99.6%; Pred. No. 3.6e-134;
 Matches 240; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSMLFYTLITAFILGIGQAEPSHSNVPAGHTTPOVHTKLQHSIDLALRRASAPAAIA 60
 DB 1 MSMLFYTLITAFILGIGQAEPSHSNVPAGHTTPOVHTKLQHSIDLALRRASAPAAIA 60
 QY 61 ARVAGQTNITVDPRLPFKKRLRSRVLFTSTQPPREADTODLDFEVGAAPFNRTHRSK 120
 DB 61 ARVAGQTNITVDPRLPFKKRLRSRVLFTSTQPPREADTODLDFEVGAAPFNRTHRSK 120
 QY 121 RSSHPITFRGEFSVCDVSVMVGDKTTATDIDIKGEVMTLGEVINNSVFKQYFFETKCR 180
 DB 121 RSSHPITFRGEFSVCDVSVMVGDKTTATDIDIKGEVMTLGEVINNSVFKQYFFETKCR 180
 QY 181 DPNPVDGCGRGIDSKHNSYCTTHTTFVKALTMDGKQAMRFIRIDTACVCLSRKAVR 240
 DB 181 DPNPVDGCGRGIDSKHNSYCTTHTTFVKALTMDGKQAMRFIRIDTACVCLSRKAVR 240
 QY 241 A 241
 DB 241 A 241

RESULT 15

AA37799 standard; Protein; 307 AA.

AC AAR37799;
 DT 29-SEP-1993 (first entry)

XX Human NGF.

KM Chimeric; human; prepro; NGF; brain-derived neurotrophic factor;
 KW BDNF; chimera; fusion; mouse; nerve growth factor; peripheral;
 XX central; precursor; nervous system.

XX Homo sapiens.

XX Key Location/Qualifiers
 FT Region 1..187
 FT /note= "Prepro region"
 FT Protein 188..307
 FT /note= "Mature NGF"

XX MO310150-A.

XX 27-MAY-1993.

XX 13-NOV-1992; 92MO-US09792.

XX 14-NOV-1991; 91US-0792492.

XX (AMGE-) AMGEN.

XX (REG-) REGENERON PHARM INC.

XX Gies D, Hu SS, Ip N, Squinto SP, Yancopoulos GD;

XX WPI; 1993-182492/22.

DR N-PSDB; AAQ42571.

XX Eukaryotic expression of neurotrophins - using prepro region of a
 PT different neurotrophin for more efficient post-translational
 PT processing

PS Disclosure; Fig 4; 80pp; English.

XX This sequence represents human nerve growth factor (NGF). The protein
 CC encoded by this sequence promotes the development of the peripheral
 CC nervous system and also influences the development and maintenance of
 CC specific populations of neurons in the central nervous system. Two
 CC major transcripts from the NGF gene result in a "long" and "short" NGF
 CC prepeptide. The "short" precursor contains a conventional signal
 CC sequence at the N-terminus which flanks the pro-region. The "long"
 CC precursor contains an additional "pro-region" at its N-terminal. No
 CC functional distinction has been elucidated between the "long" and
 CC "short" forms. Characteristics of NGF, such as isoelectric point and
 CC primary structure, are very similar to brain derived neurotrophic
 CC factor (BDNF). The NGF coding sequence may be used in the
 CC construction of a chimeric nucleic acid molecule to encode a prepro-
 CC NGF/BDNF chimera (see also AAQ42568-69).

XX Sequence 307 AA;

Query Match 99.7%; Score 1266; DB 14; Length 307;
 Best Local Similarity 99.6%; Pred. No. 5.2e-134;
 Matches 240; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSMLFYTLITAFILGIGQAEPSHSNVPAGHTTPOVHTKLQHSIDLALRRASAPAAIA 60
 DB 67 MSMLFYTLITAFILGIGQAEPSHSNVPAGHTTPOVHTKLQHSIDLALRRASAPAAIA 126
 QY 61 ARVAGQTNITVDPRLPFKKRLRSRVLFTSTQPPREADTODLDFEVGAAPFNRTHRSK 120
 DB 127 ARVAGQTNITVDPRLPFKKRLRSRVLFTSTQPPREADTODLDFEVGAAPFNRTHRSK 186
 QY 121 RSSHPITFRGEFSVCDVSVMVGDKTTATDIDIKGEVMTLGEVINNSVFKQYFFETKCR 180
 DB 187 RSSHPITFRGEFSVCDVSVMVGDKTTATDIDIKGEVMTLGEVINNSVFKQYFFETKCR 246
 QY 181 DPNPVDGCGRGIDSKHNSYCTTHTTFVKALTMDGKQAMRFIRIDTACVCLSRKAVR 240
 DB 247 DPNPVDGCGRGIDSKHNSYCTTHTTFVKALTMDGKQAMRFIRIDTACVCLSRKAVR 306
 QY 241 A 241
 DB 307 A 307

Search completed: June 6, 2003, 10:49:30
 Job time : 34.5 secs


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QY 1 MSMLFTTLITAFILIGIOAEPHSESNVPAAGHTIPQVHMTKLOHSLDTPALRRARAPAAIA 60
DB 1 MSMLFTTLITAFILIGIOAEPHSESNVPAAGHTIPQVHMTKLOHSLDTPALRRARAPAAIA 60
QY 61 ARVAGOTRNTITVDPRLFKKRLRSRVLSTOPPREAADTODLDFEVGAAPSRTHRSK 120
DB 61 ARVAGOTRNTITVDPRLFKKRLRSRVLSTOPPREAADTODLDFEVGAAPSRTHRSK 120
QY 121 RSSSHPIFRHGFSVCDVSVMWGDKTATDIDKGEVMTLGEVNNINSVFKQYFFETKCR 180
DB 121 RSSSHPIFRHGFSVCDVSVMWGDKTATDIDKGEVMTLGEVNNINSVFKQYFFETKCR 180
QY 181 DPNPVDSCGRGIDSKMNSYCTTHTFVKALTMGKQAAWRFIRIDTACVLSRKAVER 240
DB 181 DPNPVDSCGRGIDSKMNSYCTTHTFVKALTMGKQAAWRFIRIDTACVLSRKAVER 240
QY 241 A 241
DB 241 A 241

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RESULT 2

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Q9P208 PRELIMINARY; PRT; 241 AA.
ID 09P208;
AC 09P208;
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE Beta-nerve growth factor (fragment)
GN Beta-NGF
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kitano T., Kobayakawa H., Saitou N.;
RT "Silver Project.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DB EMBL; AB037517; BAA90437.1;
DR HSP; P01139; ISET.
DR InterPro; IPR02072; NGF.
DR Pfam; PF00243; NGF; 1.
DR PRINTS; PR00268; NGF.
DR ProDom; PD002052; NGF; 1.
DR SMART; SM00140; NGF; 1.
DR PROSITE; PS00248; NGF_1; 1.
DR PROSITE; PS50270; NGF_2; 1.
DR NON TER 241
SQ SEQUENCE 241 AA; 26998 MW; D531ED825D96C14 CRC64;

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Query Match 99.4%; Score 1260; DB 4; Length 241;
Best Local Similarity 99.2%; Pred. No. 9,7e-117;
Matches 239; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY 1 MSMLFTTLITAFILIGIOAEPHSESNVPAAGHTIPQVHMTKLOHSLDTPALRRARAPAAIA 60
DB 1 MSMLFTTLITAFILIGIOAEPHSESNVPAAGHTIPQVHMTKLOHSLDTPALRRARAPAAIA 60
QY 61 ARVAGOTRNTITVDPRLFKKRLRSRVLSTOPPREAADTODLDFEVGAAPSRTHRSK 120
DB 61 ARVAGOTRNTITVDPRLFKKRLRSRVLSTOPPREAADTODLDFEVGAAPSRTHRSK 120
QY 121 RSSSHPIFRHGFSVCDVSVMWGDKTATDIDKGEVMTLGEVNNINSVFKQYFFETKCR 180
DB 121 RSSSHPIFRHGFSVCDVSVMWGDKTATDIDKGEVMTLGEVNNINSVFKQYFFETKCR 180
QY 181 DPNPVDSCGRGIDSKMNSYCTTHTFVKALTMGKQAAWRFIRIDTACVLSRKAVER 240
DB 181 DPNPVDSCGRGIDSKMNSYCTTHTFVKALTMGKQAAWRFIRIDTACVLSRKAVER 240
QY 241 A 241
DB 241 A 241

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DB 241 A 241

RESULT 3

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Q96P60 PRELIMINARY; PRT; 241 AA.
ID 096P60;
AC 096P60;
DT 01-DEC-2001 (TREMblrel. 19, Created)
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
DE Nerve growth factor beta.
GN NGFB
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang Y., Zhang B., Zhou Y., Peng X., Yuan J., Qiang B.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF411526; AAL05874.1;
DR InterPro; IPR002072; NGF.
DR Pfam; PF00243; NGF; 1.
DR ProDom; PD002052; NGF; 1.
DR PROSITE; PS00248; NGF_1; UNKNOWN_1.
DR PROSITE; PS50270; NGF_2; 1.
DR PROSITE; PS50270; NGF_2; 1.
SQ SEQUENCE 241 AA; 26964 MW; 745216485C21E58 CRC64;

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Query Match

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Best Local Similarity 98.3%; Score 1253; DB 4; Length 241;
Matches 237; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

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QY 1 MSMLFTTLITAFILIGIOAEPHSESNVPAAGHTIPQVHMTKLOHSLDTPALRRARAPAAIA 60
DB 1 MSMLFTTLITAFILIGIOAEPHSESNVPAAGHTIPQVHMTKLOHSLDTPALRRARAPAAIA 60
QY 61 ARVAGOTRNTITVDPRLFKKRLRSRVLSTOPPREAADTODLDFEVGAAPSRTHRSK 120
DB 61 ARVAGOTRNTITVDPRLFKKRLRSRVLSTOPPREAADTODLDFEVGAAPSRTHRSK 120
QY 121 RSSSHPIFRHGFSVCDVSVMWGDKTATDIDKGEVMTLGEVNNINSVFKQYFFETKCR 180
DB 121 RSSSHPIFRHGFSVCDVSVMWGDKTATDIDKGEVMTLGEVNNINSVFKQYFFETKCR 180
QY 181 DPNPVDSCGRGIDSKMNSYCTTHTFVKALTMGKQAAWRFIRIDTACVLSRKAVER 240
DB 181 DPNPVDSCGRGIDSKMNSYCTTHTFVKALTMGKQAAWRFIRIDTACVLSRKAVER 240
QY 241 A 241
DB 241 A 241

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RESULT 4

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Q9N2F0 PRELIMINARY; PRT; 241 AA.
ID 09N2F0;
AC 09N2F0;
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE Beta-nerve growth factor (fragment)
GN Beta-NGF
OS Gorilla gorilla (gorilla)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
OX NCBI_TaxId=9593;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=GORILLA-UI;
RA Kitano T., Kobayakawa H., Saitou N.;
RT "Silver Project.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB037519; BAA90439.1;

```

DR HSSP; P01139; 1BET.
 DR InterPro; IPR002072; NGF.
 DR Pfam; PF00243; NGF; 1.
 DR PRINTS; PR00268; NGF.
 DR ProDom; PD002052; NGF; 1.
 DR SMART; SM00140; NGF; 1.
 DR PROSITE; PS00248; NGF; 1; 1.
 DR PROSITE; PS50270; NGF; 2; 1.
 DR NON TER 241
 FT 241
 SQ SEQUENCE 241 AA; 26915 MW; 6F54D163C364B34 CRC64;

Query Match 98.1%; Score 1244; DB 6; Length 241;
 Best Local Similarity 98.3%; Pred. No. 3.7e-115;
 Matches 236; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MSMLFYTLITAFILGIGQAEHPSBSNVPAAGHTIPQAHWTKLQHSIDTLARRASAPAAIA 60
 DB 1 MSMLFYTLITAFILGIGQAEHPSBSNVPAAGHTIPQAHWTKLQHSIDTLARRASAPAAIA 60
 QY 61 ARVAGQTNITVDPRLFKRRRLSPRVLFSTQPPRAADTODLDFEVGAAPFRTSRK 120
 DB 61 ARVAGQTNITVDPRLFKRRRLSPRVLFSTQPPRAADTODLDFEVGAAPFRTSRK 120
 QY 121 RSSSHPIFRHGSEFVCDVSVMVGDKTATADIKGEVWVLGEVINNSVFKQYFFETKCR 180
 DB 121 RSSSHPIFRHGSEFVCDVSVMVGDKTATADIKGEVWVLGEVINNSVFKQYFFETKCR 180
 QY 181 DENPVDGCGRIGDSKHMNSYCTTHTFVKALTMGKQAMRFIRIDTACVLSRAVRR 240
 DB 181 DENPVDGCGRIGDSKHMNSYCTTHTFVKALTMGKQAMRFIRIDTACVLSRAVRR 240
 QY 241 A 241
 DB 241 A 241

RESULT 5

Q9N2F1 PRELIMINARY; PRT; 241 AA.
 AC Q9N2F1;
 DT 01-OCT-2000 (TREMblrel. 15, Created)
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE Beta-nerve growth factor (Fragment).
 GN BETA-NGF.
 OS Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
 RN NCBI_TaxID=9598;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CHIMP-220;
 RA Kitano T., Kobayakawa H., Satou N.,
 RT "Silver Project".
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB037518; BAA90438.1; -
 DR HSSP; P01139; 1BET.
 DR InterPro; IPR002072; NGF.
 DR Pfam; PF00243; NGF; 1.
 DR PRINTS; PR00268; NGF.
 DR ProDom; PD002052; NGF; 1.
 DR SMART; SM00140; NGF; 1.
 DR PROSITE; PS00248; NGF; 1; 1.
 DR PROSITE; PS50270; NGF; 2; 1.
 DR NON TER 241
 FT 241
 SQ SEQUENCE 241 AA; 26868 MW; B39FAA8912C00A0B CRC64;

Query Match 98.0%; Score 1243; DB 6; Length 241;
 Best Local Similarity 97.9%; Pred. No. 4.7e-115;
 Matches 236; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MSMLFYTLITAFILGIGQAEHPSBSNVPAAGHTIPQAHWTKLQHSIDTLARRASAPAAIA 60
 DB 1 MSMLFYTLITAFILGIGQAEHPSBSNVPAAGHTIPQAHWTKLQHSIDTLARRASAPAAIA 60

DB 1 MSMLFYTLITAFILGIGQAEHPSBSNVPAAGHTIPQAHWTKLQHSIDTLARRASAPAAIA 60
 QY 61 ARVAGQTNITVDPRLFKRRRLSPRVLFSTQPPRAADTODLDFEVGAAPFRTSRK 120
 DB 61 ARVAGQTNITVDPRLFKRRRLSPRVLFSTQPPRAADTODLDFEVGAAPFRTSRK 120
 QY 121 RSSSHPIFRHGSEFVCDVSVMVGDKTATADIKGEVWVLGEVINNSVFKQYFFETKCR 180
 DB 121 RSSSHPIFRHGSEFVCDVSVMVGDKTATADIKGEVWVLGEVINNSVFKQYFFETKCR 180
 QY 181 DENPVDGCGRIGDSKHMNSYCTTHTFVKALTMGKQAMRFIRIDTACVLSRAVRR 240
 DB 181 DENPVDGCGRIGDSKHMNSYCTTHTFVKALTMGKQAMRFIRIDTACVLSRAVRR 240
 QY 241 A 241
 DB 241 A 241

RESULT 6

Q9N2E9 PRELIMINARY; PRT; 241 AA.
 AC Q9N2E9;
 DT 01-OCT-2000 (TREMblrel. 15, Created)
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE Beta-nerve growth factor (Fragment).
 GN BETA-NGF.
 OS Pongo pygmaeus (Orangutan).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
 RN NCBI_TaxID=9600;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ORAN-U1;
 RA Kitano T., Kobayakawa H., Satou N.,
 RT "Silver Project".
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB037520; BAA90440.1; -
 DR HSSP; P01139; 1BET.
 DR InterPro; IPR002072; NGF.
 DR Pfam; PF00243; NGF; 1.
 DR PRINTS; PR00268; NGF.
 DR ProDom; PD002052; NGF; 1.
 DR SMART; SM00140; NGF; 1.
 DR PROSITE; PS00248; NGF; 1; 1.
 DR PROSITE; PS50270; NGF; 2; 1.
 DR NON TER 241
 FT 241
 SQ SEQUENCE 241 AA; 26876 MW; DEC168E7B4E01F15 CRC64;

Query Match 97.9%; Score 1242; DB 6; Length 241;
 Best Local Similarity 97.9%; Pred. No. 5.9e-115;
 Matches 236; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MSMLFYTLITAFILGIGQAEHPSBSNVPAAGHTIPQAHWTKLQHSIDTLARRASAPAAIA 60
 DB 1 MSMLFYTLITAFILGIGQAEHPSBSNVPAAGHTIPQAHWTKLQHSIDTLARRASAPAAIA 60
 QY 61 ARVAGQTNITVDPRLFKRRRLSPRVLFSTQPPRAADTODLDFEVGAAPFRTSRK 120
 DB 61 ARVAGQTNITVDPRLFKRRRLSPRVLFSTQPPRAADTODLDFEVGAAPFRTSRK 120
 QY 121 RSSSHPIFRHGSEFVCDVSVMVGDKTATADIKGEVWVLGEVINNSVFKQYFFETKCR 180
 DB 121 RSSSHPIFRHGSEFVCDVSVMVGDKTATADIKGEVWVLGEVINNSVFKQYFFETKCR 180
 QY 181 DENPVDGCGRIGDSKHMNSYCTTHTFVKALTMGKQAMRFIRIDTACVLSRAVRR 240
 DB 181 DENPVDGCGRIGDSKHMNSYCTTHTFVKALTMGKQAMRFIRIDTACVLSRAVRR 240
 QY 241 A 241
 DB 241 A 241

RESULT 7

Q9N183

PRELIMINARY; PRT; 217 AA.

AC Q9N183; 01-OCT-2000 (Tremblrel. 15, Created)

DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)

DE 01-DEC-2001 (Tremblrel. 19, Last annotation update)

OS Macaca fuscata (Japanese macaque)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;

OC Cercopithecoidea; Macaca.

OX NCBI_Taxid=9542;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=BLOOD;

RX MEDLINE=99270338; PubMed=10340513;

RA Okuno H., Tokuyama W., Li Y.X., Hashimoto T., Miyashita Y.;

RT "Quantitative evaluation of neurotrophin and trk mRNA expression in

RT visual and limbic areas along the occipito-temporo-hippocampal pathway

RT in adult macaque monkeys."

RT J. Comp. Neurol. 408:378-398 (1999).

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=BLOOD;

RX Okuno H., Tokuyama W., Li Y.X., Hashimoto T., Miyashita Y.;

RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF222682; AAF33790.1; -

DR HSP; P01139; 1BET.

DR InterPro; IPRO02072; NGF.

DR Pfam; PF00243; NGF; 1.

DR PRINTS; PR00252; NGF; 1.

DR ProDom; PD002052; NGF; 1.

DR SMART; SM00140; NGF; 1.

DR PROSITE; PS00248; NGF; 1.

DR PROSITE; PS00270; NGF; 2; 1.

FT NON_TER

SQ SEQUENCE 217 AA; 24240 MW; 36A5A2D1DFC8D5C CRC64;

Query Match

Best Local Similarity 97.7%; Score 1127; DB 6; Length 217;

Matches 212; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 11 AFLIGIOABPHSESVNPAAGHTIPQVHTKLOHSLDTALRRASAPAAIAARVAGQTN

DB 1 AFLIGIOABPHSESVNPAAGHTIPQVHTKLOHSLDTALRRASAPAAIAARVAGQTN

QY 71 TVDPLFKKRLRSRVLFTSTPPPEADTODLDFEVGGAAPFSTHRSKSSSHPIFHR

DB 61 TVDPLFKKRLRSRVLFTSTPPPEADTODLDFEVGGAAPFSTHRSKSSSHPIFHR

QY 131 GEFVSVVWVGDKTATDIDIKGEVAVLGEVININSVFPQYFETCRDPNPVDSGR

DB 121 GEFVSVVWVGDKTATDIDIKGEVAVLGEVININSVFPQYFETCRDPNPVDSGR

QY 191 GIDSKHNSYCTTHTTFYKALTMGKQAMRFIRIDT

DB 181 GIDSKHNSYCTTHTTFYKALTMGKQAMRFIRIDT

QY 227

DB 217

QY 181

DB 217

QY 217

DB 217

QY 217

DB 217

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;

RP SEQUENCE FROM N.A.
 RC TISSUE=Salivary Gland;
 RA Strausberg R.;

RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC011123; AAH11123.1; -

DR MGD; MGI:97321; NGF.

DR InterPro; IPRO02072; NGF.

DR Pfam; PF00243; NGF; 1.

DR ProDom; PD002052; NGF; 1.

DR PROSITE; PS00248; NGF; 1; UNKNOWN_1.

DR PROSITE; PS00270; NGF; 2; 1.

DR PROSITE; PS00270; NGF; 2; 1.

DR PROSITE; PS00270; NGF; 2; 1.

DR PROSITE; PS00270; NGF; 2; 1.

DR PROSITE; PS00270; NGF; 2; 1.

DR PROSITE; PS00270; NGF; 2; 1.

DR PROSITE; PS00270; NGF; 2; 1.

DR PROSITE; PS00270; NGF; 2; 1.

DR PROSITE; PS00270; NGF; 2; 1.

DR PROSITE; PS00270; NGF; 2; 1.

DR PROSITE; PS00270; NGF; 2; 1.

DR PROSITE; PS00270; NGF; 2; 1.

DR PROSITE; PS00270; NGF; 2; 1.

DR PROSITE; PS00270; NGF; 2; 1.

DR PROSITE; PS00270; NGF; 2; 1.

DR PROSITE; PS00270; NGF; 2; 1.

DR PROSITE; PS00270; NGF; 2; 1.

DR PROSITE; PS00270; NGF; 2; 1.

DR PROSITE; PS00270; NGF; 2; 1.

DR PROSITE; PS00270; NGF; 2; 1.

DR PROSITE; PS00270; NGF; 2; 1.

DR PROSITE; PS00270; NGF; 2; 1.

DR PROSITE; PS00270; NGF; 2; 1.

DR PROSITE; PS00270; NGF; 2; 1.

DR PROSITE; PS00270; NGF; 2; 1.

DR PROSITE; PS00270; NGF; 2; 1.

DR PROSITE; PS00270; NGF; 2; 1.

DR PROSITE; PS00270; NGF; 2; 1.

DR PROSITE; PS00270; NGF; 2; 1.

DR PROSITE; PS00270; NGF; 2; 1.

Query Match

Best Local Similarity 84.2%; Score 1033; DB 11; Length 294;

Matches 192; Conservative 15; Mismatches 21; Indels 0; Gaps 0;

QY 1 MSMLFYTLITAFILGIOABPHSESVNPAAGHTIPQVHTKLOHSLDTALRRASAPAAIA

DB 67 MSMLFYTLITAFILGIOABPHSESVNPAAGHTIPQVHTKLOHSLDTALRRASAPAAIA

QY 61 ARVAGQTNITVDRLFKKRLRSRVLFTSTPPPEADTODLDFEVGGAAPFSTHRSK

DB 127 ARVAGQTNITVDRLFKKRLRSRVLFTSTPPPEADTODLDFEVGGAAPFSTHRSK

QY 121 RSSHPIFHRGEPFVSVWVGDKTATDIDIKGEVAVLGEVININSVFPQYFETCR

DB 187 RSSHPIFHRGEPFVSVWVGDKTATDIDIKGEVAVLGEVININSVFPQYFETCR

QY 181 DPNVDSGRCGIDSKHNSYCTTHTTFYKALTMGKQAMRFIRIDT

DB 247 ASNPVDSGRCGIDSKHNSYCTTHTTFYKALTMGKQAMRFIRIDT

QY 228

DB 294

QY 294

DB 294

QY 294

DB 294

QY 294

DB 294

QY 294

DB 294

QY 294

DB 294

QY 294

DB 294

QY 294

DB 294

QY 294

DB 294

QY 294

DB 294

QY 294

DB 294

QY 294

DB 294

QY 294

DB 294

QY 294

DB 294

QY 1 MSMLFTLLITAFLLIGIAEPHSESNYPAG----HTIPQVMTQLQSLDTALRARSADA 56
 DB 1 MSMLCTLLIIAFLIGIWAAPKSEDNVPLSPATSDLSCKATHALAKTSRNIIDHICA 60
 QY 57 AAIWA-RVAGGOTRNTVVDRLPKKRLRSPRYLFTSTPPREAADTODLDFEYGAAPSR 115
 DB 61 PKKAEDEFGSAANIIVDPKLFQKRRFQSPRYLFTSTPPRLSRDEQSV-----NANSLNR 116
 QY 116 TRSKRSSHPHFHGEFVSCDSVAVVGDKTATDIDKKEVWVGLGEVNNINSVFKQYFF 175
 DB 117 NTRAKR-EDHPFHAKGEYSVCSVAVVANKTATIDIRGLVTVVAVVNNVNYKQYFF 175
 QY 176 ETKCRDPNVDGCRGIDSKHNSYCTTHTTFVKALTMDDKQAAWRFIRIDPACVLSR 235
 DB 176 ETKCRDPNVPVPGCGIGIDARHNSYCTTNTTFVKALTMGNGQASWRFIRIDACVLSR 235
 QY 236 K 236
 DB 236 K 236

RESULT 10

Q90W38 PRELIMINARY; PRT; 241 AA.
 AC Q90W38;
 DT 01-DEC-2001 (TRENBLrel. 19, Created)
 DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)
 DB Putative neurotrophic growth factor.
 NGF.
 OS Bothrops jararacusu (Jararacusu).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidae;
 OC Viperidae; Crotalinae; Bothrops.
 NCBI_TaxID=8726;
 CX NCBI_TaxID=8726;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=VENOM GLAND;
 RA Kashima S., Pereira J.O., Astolfi Filho S., Soares A.M.,
 RA Catriera A.C.O., Giglio J.R., Franca S.C.;
 RA "Molecular cloning and cDNA sequence of a nerve growth factor
 precursor from Bothrops jararacusu venomous gland."
 RL Submitted (AUG-2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AY007318; AAG12169.1;
 DR InterPro; IPR002072; NGF.
 DR Pfam; PF00243; NGF; 1.
 DR ProDom; PD002052; NGF; 1.
 DR PROSITE; PS00248; NGF_1; UNKNOWN_1.
 DR PROSITE; PS0270; NGF_2; 1.
 SQ SEQUENCE 241 AA; 27161 MW; ACS7F724A6531A8F CRC64;

Query Match 55.5%; Score 704; DB 13; Length 241;
 Best Local Similarity 58.9%; Pred. No. 1.2e-61;
 Matches 142; Conservative 30; Mismatches 59; Indels 10; Gaps 4;

QY 1 MSMLFTLLITAFLLIGIAEPHSESNYPAG----HTIPQVMTQLQSLDTALRARSADA 56
 DB 1 MSMLCTLLIIAFLIGIWAAPKSEDNVPLSPATSDLSCKATHALAKTSRNIIDHICA 60
 QY 57 AAIWA-RVAGGOTRNTVVDRLPKKRLRSPRYLFTSTPPREAADTODLDFEYGAAPSR 115
 DB 61 PKKAEDEFGSAANIIVDPKLFQKRRFQSPRYLFTSTPPRLSRDEQSV-----DANSLNR 116
 QY 116 TRSKRSSHPHFHGEFVSCDSVAVVGDKTATDIDKKEVWVGLGEVNNINSVFKQYFF 175
 DB 117 NTRAKR-EDHPFHAKGEYSVCSVAVVANKTATIDIRGLVTVVAVVNNVNYKQYFF 175
 QY 176 ETKCRDPNVDGCRGIDSKHNSYCTTHTTFVKALTMDDKQAAWRFIRIDPACVLSR 235
 DB 176 ETKCRDPNVPVPGCGIGIDARHNSYCTTNTTFVKALTMGNGQASWRFIRIDACVLSR 235
 QY 236 K 236

DB 236 K 236

RESULT 11

Q9PTC3 PRELIMINARY; PRT; 87 AA.
 AC Q9PTC3;
 DT 01-MAY-2000 (TRENBLrel. 13, Created)
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
 DE Beta nerve growth factor (Fragment).
 NGF.
 OS Cerus elaphus scoticus.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Kumlantia; Pecora; Cervoidae;
 OC Cervidae; Cervinae; Cervus.
 NCBI_TaxID=109627;
 CX NCBI_TaxID=109627;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Robertson T.M., Stanton J.L., Clark D.E., Sheard P.W., Harris A.J.,
 RA Suttie J.M.;
 RA "NGF expression in Antler."
 RT Submitted (Apr-1999) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AF145043; AAF17235.1;
 DR HSSP; P01139; 1BET.
 DR InterPro; IPR002072; NGF.
 DR Pfam; PF00243; NGF; 1.
 DR PRINTS; PR00268; NGF.
 DR ProDom; PD002052; NGF; 1.
 DR SMART; SMO0140; NGF; 1.
 DR PROSITE; PS00248; NGF_1; 1.
 DR PROSITE; PS0270; NGF_2; 1.
 FT NON_TER 1
 FT NON_TER 87
 SQ SEQUENCE 87 AA; 9876 MW; 17E06E49A7A0A4 CRC64;

Query Match 36.4%; Score 462; DB 6; Length 87;
 Best Local Similarity 36.6%; Pred. No. 3.1e-38;
 Matches 84; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 138 SVSVVGDKTATDIDKKEVWVGLGEVNNINSVFKQYFFETKCRDPNVPVDSGCRGIDSKW 197
 DB 1 SVSVVGDKTATDIDKKEVWVGLGEVNNINSVFKQYFFETKCRDPNVPVDSGCRGIDSKW 60
 QY 198 NSYCTTHTTFVKALTMDDKQAAWRFIR 224
 DB 61 NSYCTTHTTFVKALTMDDKQAAWRFIR 87

RESULT 12

Q9P224 PRELIMINARY; PRT; 87 AA.
 AC Q9P224;
 DT 01-OCT-2000 (TRENBLrel. 15, Created)
 DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
 DE Truncated beta nerve growth factor (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 CX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=95236507; Pubmed=7720122;
 RA Li Y., Huang B., Cai L.;
 RA "Amplification, cloning and sequencing of beta nerve growth factor
 gene in the Chinese population."
 RL Chung-Kuo I Hsueh Ko Hsueh Yuan Hsueh Pao 16:334-338 (1994).
 DR EMBL; S76884; AAB34114.2;
 DR HSSP; P01139; 1BET.
 DR InterPro; IPR002072; NGF.
 DR Pfam; PF00243; NGF; 1.
 DR PRINTS; PR00268; NGF.

DR ProdDom; PD002052; NGF; 1.
 DR SMART; SM00140; NGF; 1.
 DR PROSITE; PS50270; NGF_2; 1.
 FT NON TER 1
 SQ SEQUENCE 87 AA; 9729 MW; 45E9E27386FDEB27 CRC64;

Query Match 36.2%; Score 459; DB 4; Length 87;
 Best Local Similarity 94.3%; Pred. No. 6.2e-38;
 Matches 82; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 122 SSSHPFHGGEFVCDVSVWVGDKTTATDICKEMVLTGERVNNVSKQFFETKCRD 181
 DB 1 SSSHPFHGGEFVCDVSVWVGDKTTATDICKEMVLTGERVNNVSKQFFETKCRD 60

QY 182 PNPVDSGCGRIDSKHNSYCTTHFEV 208
 DB 61 PNPVDSGCGRIDSKHNSYCTTHFEV 87

RESULT 13
 Q9WU15 PRELIMINARY; PRT; 132 AA.

DT 01-NOV-1999 (TREMBlrel. 12, Created)
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Nerve growth factor (Fragment).
 OS Mesocricetus auratus (Golden hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Mesocricetus.
 OX NCBI_TaxID=10036;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Tansen H.T., Lehman M.N., Stevens P.J.;
 RT "Golden Hamster Neurotrophin and Neurotrophin Receptor cDNA";
 RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF104239; AAD21010.1; -
 FT NON TER 1
 FT NON TER 132
 SQ SEQUENCE 132 AA; 14649 MW; 0C36B6283225DA6 CRC64;

Query Match 35.1%; Score 444.5; DB 11; Length 132;
 Best Local Similarity 74.6%; Pred. No. 2.8e-36;
 Matches 88; Conservative 11; Mismatches 18; Indels 1; Gaps 1;

QY 1 MSMLFYTLITAFILGIOAEPHSESVNPAHGHTIPQVHTKLGHSIDTALRRARAPAAIA 60
 DB 16 MSMLFYTLITAFILGVOAEPYTDSTVPGSDSVPOAHMTKLOHSYDTALRRARAPAGASIA 75
 QY 61 ARVAGQTNITVDPFLFKKRLRSPRVLFSTQPREADTODLOPEVGGAAPFGRTR 118
 DB 76 ARVAGQTNITVDPFLFKKRLRSPRVLFSTQPREADTODLOPEVGGAAPFGRTR 132

RESULT 14
 Q91988 PRELIMINARY; PRT; 286 AA.

DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE Neurotrophin-6 precursor.
 OS Xiphophorus maculatus (Southern platyfish), and
 OS Xiphophorus helleri.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorphi; Acanthopterygii; Perciformes; Atherinomorpha;
 OC Cyprinodontiformes; Poeciliidae; Xiphophorus.
 OX NCBI_TaxID=8083, 8084;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95059452; PubMed=7969471;

RA Gotz R., Koster R., Winkler C., Raulf F., Lottepeich F., Scharl M.,
 RA Thoenen H.;
 RT "Neurotrophin-6 is a new member of the nerve growth factor family";
 RL Nature 372:266-269(1994).
 DR EMBL; U36942; AAA61923.1; -
 DR EMBL; U36925; AAA61922.1; -
 DR EMBL; U36926; AAA61921.1; -
 DR HSSP; P01139; IBER.
 DR InterPro; IPR002072; NGF.
 DR Pfam; PF00243; NGF; 1.
 DR PRINTS; PR00268; NGF.
 DR ProdDom; PD002052; NGF; 1.
 DR SMART; SM00140; NGF; 1.
 DR PROSITE; PS00248; NGF_1; 1.
 DR PROSITE; PS50270; NGF_2; 1.
 FT Signal.
 FT SIGNAL 1 142
 FT CHAIN 143 286
 SQ SEQUENCE 286 AA; 31424 MW; 5607DBA6792E12D CRC64;

Query Match 33.6%; Score 426; DB 13; Length 286;
 Best Local Similarity 38.6%; Pred. No. 5.1e-34;
 Matches 110; Conservative 31; Mismatches 84; Indels 60; Gaps 10;

QY 8 LITAFILGIOAEPHSESVNPAHGHTIPQVHTKLGHSIDTALRRARAPAAIA 51
 DB 6 LITAFILGVOAEPYTDSTVPGSDSVPOAHMTKLOHSYDTALRRARAPAGASIA 65
 QY 52 RSAPAA-----IAAVAGQTNITVDPFLFKKRLRSPRVLFSTQPREADTODLOPEVGGAAPFGRTR 98
 DB 66 RTGSAAGNMQNRTVIGPSPAGSSPVPDVKLPKSHYRSPVVFSEVPSHDVL 125
 QY 99 DTQDLDFE-VGGAAPFGRTRSKSSHPFHGGEFVCDVSVWVGDKTTATDICKEMV 157
 DB 126 DGEYDDEERVGL-----RVKRAVSHTHRGEVSCDSINTW-NKTRATMDSGNEV 177
 QY 158 MVLGAEVNNVSVFQYFETKCRD-----NPDVSGCGRIDSK 195
 DB 178 TVLSHTVNNKVKQKLPFETTCGSPTRSSGIVYGSGRGKQSGKRTGNSGCGRIDSK 237
 QY 196 HNSVYCTTHHTFVKALTMDSKQAAWPRIRIDTACVLSRAVVR 240
 DB 238 YNNSHCNTNDIYVSLTVFKEQTAMRIRINACVLSRNSWR 282

RESULT 15
 Q9N182 PRELIMINARY; PRT; 241 AA.

DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Neurotrophin-3 (Fragment).
 OS Macaca fuscata (Japanese macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Macaca.
 OX NCBI_TaxID=9542;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BLOOD;
 RX MEDLINE=99270338; PubMed=10340513;
 RA Okuno H., Tokuyama W., Li Y.X., Hashimoto T., Miyashita Y.;
 RT "Quantitative evaluation of neurotrophin and trk mRNA expression in
 RT visual and limbic areas along the occipito-temporo-hippocampal pathway
 RT in adult macaque monkeys";
 RL J. Comp. Neurol. 408:378-396(1999).
 RN [2]

RP SEQUENCE FROM N.A.
 RC TISSUE=BLOOD;
 RA Hashimoto T., Okuno H., Tokuyama W., Li Y.X., Miyashita Y.;
 RT "Expression of brain-derived neurotrophic factor, neurotrophin-3 and
 RT their receptor messenger RNAs in monkey rhinal cortex";

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OM protein - protein search, using sw model

Run on: June 6, 2003, 10:47:02 ; Search time 9 seconds
(without alignments)
1110.644 Million cell updates/sec

Title: US-09-788-188-2
Perfect score: 1268
Sequence: 1 MSMTFTLITAFILIGIQAF.....FRIIDTACVCLSRKAVRRA 241

Scoring table: BIOSIM62
Gapop 10.0, Gapext 0.5

Searched: 112892 seqs, 41476328 residues
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1265	99.8	241	1	NGF_HUMAN
2	1119	88.2	229	1	NGF_PIG
3	1102	86.9	241	1	NGF_BOVIN
4	1101	86.8	231	1	NGF_MOUSE
5	1091	86.0	241	1	NGF_MOUSE
6	1087	85.7	241	1	NGF_MOUSE
7	1068	84.2	241	1	NGF_MOUSE
8	783.5	61.8	241	1	NGF_MOUSE
9	768	60.6	231	1	NGF_MOUSE
10	671.5	53.0	243	1	NGF_MOUSE
11	484	38.2	117	1	NGF_MOUSE
12	481.5	38.0	194	1	NGF_MOUSE
13	476.5	37.6	257	1	NGF_MOUSE
14	469	37.0	260	1	NGF_MOUSE
15	468.5	36.9	257	1	NGF_MOUSE
16	467	36.8	258	1	NGF_MOUSE
17	466.5	36.8	257	1	NGF_MOUSE
18	465	36.2	258	1	NGF_MOUSE
19	459.5	35.4	233	1	NGF_MOUSE
20	449.5	35.4	116	1	NGF_MOUSE
21	445.5	35.1	116	1	NGF_MOUSE
22	372.5	29.4	140	1	NGF_MOUSE
23	365	28.8	247	1	NGF_MOUSE
24	364	28.7	249	1	NGF_MOUSE
25	363	28.6	255	1	NGF_MOUSE
26	362	28.5	247	1	NGF_MOUSE
27	361	28.5	247	1	NGF_MOUSE
28	361	28.5	247	1	NGF_MOUSE
29	360	28.4	249	1	NGF_MOUSE
30	358.5	28.3	252	1	NGF_MOUSE
31	350	27.6	247	1	NGF_MOUSE
32	348.5	27.5	248	1	NGF_MOUSE
33	347.5	27.4	246	1	NGF_MOUSE

ALIGNMENTS

34	338	26.7	236	1	NT4_XENLA	P24727 xenopus lae
35	336.5	26.5	270	1	BDNF_CYPRA	Q09022 cyprinus ca
36	335	26.4	269	1	BDNF_XIPMA	Q02193 xiphophorus
37	332.5	26.2	210	1	NT5_HUMAN	P34131 homo sapien
38	325.5	25.7	209	1	NT5_RAT	P34131 rattus norv
39	323.5	25.5	114	1	BDNF_MACMU	Q06225 macaca mla
40	307.5	24.3	114	1	BDNF_XENLA	P25432 xenopus lae
41	230	18.1	257	1	NT6B_HUMAN	P34133 homo sapien
42	227	17.9	257	1	NT6A_HUMAN	P34132 homo sapien
43	226	17.8	186	1	NT6G_HUMAN	P34134 homo sapien
44	190	15.0	42	1	NGF_VIPER	P25428 vipera lebe
45	139	11.0	154	1	NT3_CEREL	Q95150 cervus elap

RESULT 1
ID NGF_HUMAN STANDARD, PRT, 241 AA.
AC NGF_HUMAN
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Beta-nerve growth factor precursor (Beta-NGF).
GN NGF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
CX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83244969; PubMed=6688123;
RA Ullrich A., Gray A., Berman C., Dull T.J.;
RT "Human beta-nerve growth factor gene sequence highly homologous to
RT that of mouse.";
RL Nature 303:821-825(1983).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=84206565; PubMed=6327169;
RA Ullrich A., Gray A., Berman C., Coussens L., Dull T.J.;
RT "Sequence homology of human and mouse beta-NGF subunit genes.";
RL Cold Spring Harb. Symp. Quant. Biol. 48:435-442(1983).
RN [3]
RP SEQUENCE FROM N.A.
RX TISSUE=Brain;
RA MEDLINE=90326556; PubMed=2374737;
RA Borsani G., Pizzuti A., Ruggeri F.E.;
RT "CDNA sequence of human beta-NGF.";
RL Nucleic Acids Res. 18:4020-4020(1990).
RN [4]
RP SEQUENCE OF 178-219 FROM N.A.
RX TISSUE=Leukocyte;
RA MEDLINE=9122573; PubMed=2025430;
RA Hallboeck F., Ibanez C.F., Persson H.;
RT "Evolutionary studies of the nerve growth factor family reveal a
RT novel member abundantly expressed in Xenopus ovary.";
RL Neuron 6:845-858(1991).
RN [5]
RP FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
RP MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT
RP STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
RP EMBRYONIC SENSORY NEURONS.
RN [6]
RP SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
RN [7]
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CC EMBL: VO1511; CAA24755.1; -
 DR EMBL: M21062; AA59931.1; -
 DR EMBL: X52599; CAA36832.1; -
 DR PIR: A01399; NGHDM.
 DR PIR: S10253; S10253.
 DR HSP: P01139; 1BET.
 DR Genew: HGNC:7808; NGFB.
 DR MIM: 162030; -
 DR InterPro: IPR002072; NGF.
 DR Pfam: PF00243; NGF; 1.
 DR PRINTS: PR00268; NGF.
 DR ProDom: PD002052; NGF; 1.
 DR SMART: SM00140; NGF; 1.
 DR PROSITE: PS00248; NGF; 1.
 DR PROSITE: PS50270; NGF; 2; 1.
 DR Growth factor; Signal.
 KM SIGNAL 1 18
 FT PROPEP 19 121
 FT CHAIN 122 241
 FT DISULFID 136 201
 FT DISULFID 179 229
 FT DISULFID 189 231
 FT CARBOHYD 69 69
 FT CARBOHYD 114 114
 SQ SEQUENCE 241 AA; 26987 MW; CFI8B4DCB736B0F CRC64;

Query Match 99.8%; Score 1265; DB 1; Length 241;
 Best Local Similarity 99.6%; Pred. No. 1.3e-112;
 Matches 240; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSMTPLYTLTFLGIGOEPESESNVPAAGHTIPQVHTKLOHSLDTLRARSPAPAAIA 60
 DB 1 MSMTPLYTLTFLGIGOEPESESNVPAAGHTIPQVHTKLOHSLDTLRARSPAPAAIA 60
 QY 61 ARVAGOTRNITVDPRLFKKRLRSRPRVLFSTQPPREADTDODLPEVGAAPFGRTRSK 120
 DB 61 ARVAGOTRNITVDPRLFKKRLRSRPRVLFSTQPPREADTDODLPEVGAAPFGRTRSK 120
 QY 121 RSSHPIFHNGEFCVSVSWVGDKTATDIDKEVWVIGEVNINNSVFQYFFETKCR 180
 DB 121 RSSHPIFHNGEFCVSVSWVGDKTATDIDKEVWVIGEVNINNSVFQYFFETKCR 180
 QY 181 DPNVDSGCRGIDSKHNSYCTTHTFVKALTMGKQANRFIRIDTACVLSRKAVRR 240
 DB 181 DPNVDSGCRGIDSKHNSYCTTHTFVKALTMGKQANRFIRIDTACVLSRKAVRR 240
 QY 241 A 241
 DB 241 A 241

RESULT 2
 NGF_PIG STANDARD; PRT; 229 AA.
 AC Q29074;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Beta-nerve growth factor precursor (Beta-NGF) (Fragment).
 GN NGFB.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
 OC NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Large white; TISSUE=Blood;
 RX MEDLINE=94313891; PubMed=8039422;
 RA Labbb-Mansais Y., Mellink C., Yerde M., Gellin J.,
 RT "A new marker (NGFB) on pig chromosome 4, isolated by using a
 RT consensus sequence conserved among species";
 RL Cytogenet. Cell Genet. 67:120-125 (1994).

CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
 CC MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT
 CC STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
 CC EMBRYONIC SENSORY NEURONS.
 CC -1- SUBUNIT: HOMODIMER, ASSOCIATED BY NONCOVALENT FORCES.
 CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
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 CC or send an email to license@1sb-sib.ch).

CC EMBL: L31898; AAA21301.1; -
 DR HSP: P01139; 1BET.
 DR InterPro: IPR002072; NGF.
 DR Pfam: PF00243; NGF; 1.
 DR ProDom: PD002052; NGF; 1.
 DR SMART: SM00140; NGF; 1.
 DR PROSITE: PS00248; NGF; 1.
 DR PROSITE: PS50270; NGF; 2; 1.
 KM Growth factor; Signal.
 FT NON_TER 1 1
 FT SIGNAL <1 6
 FT PROPEP 7 109
 FT CHAIN 110 229
 FT DISULFID 124 189
 FT DISULFID 167 217
 FT DISULFID 177 219
 FT CARBOHYD 57 57
 FT CARBOHYD 102 102
 FT CARBOHYD 154 154
 SQ SEQUENCE 229 AA; 25275 MW; FE8890771CEA3189 CRC64;

Query Match 88.2%; Score 1119; DB 1; Length 229;
 Best Local Similarity 92.1%; Pred. No. 8.2e-99;
 Matches 211; Conservative 5; Mismatches 13; Indels 0; Gaps 0;

QY 13 LIGIOEPESESNVPAAGHTIPQVHTKLOHSLDTLRARSPAPAAIAARVAGOTRNITV 72
 DB 1 LIGIOEPESESNVPAAGHTIPQVHTKLOHSLDTLRARSPAPAAIAARVAGOTRNITV 72
 QY 73 DPLFKKRLRSRPRVLFSTQPPREADTDODLPEVGAAPFGRTRSKSSHPFHGR 132
 DB 73 DPLFKKRLRSRPRVLFSTQPPREADTDODLPEVGAAPFGRTRSKSSHPFHGR 132
 QY 61 DPLFKKRLRSRPRVLFSTQPPREADTDODLPEVGAAPFGRTRSKSSHPFHGR 120
 DB 61 DPLFKKRLRSRPRVLFSTQPPREADTDODLPEVGAAPFGRTRSKSSHPFHGR 120
 QY 133 FSVCDSSVWVGDKTATDIDKEVWVIGEVNINNSVFQYFFETKCRDPNPVDSGCRGI 192
 DB 133 FSVCDSSVWVGDKTATDIDKEVWVIGEVNINNSVFQYFFETKCRDPNPVDSGCRGI 192
 QY 121 FSVCDSSVWVGDKTATDIDKEVWVIGEVNINNSVFQYFFETKCRDPNPVDSGCRGI 180
 DB 121 FSVCDSSVWVGDKTATDIDKEVWVIGEVNINNSVFQYFFETKCRDPNPVDSGCRGI 180
 QY 193 DSKHNSYCTTHTFVKALTMGKQANRFIRIDTACVLSRKAVRR 241
 DB 193 DSKHNSYCTTHTFVKALTMGKQANRFIRIDTACVLSRKAVRR 241

RESULT 3
 NGF_RAT STANDARD; PRT; 241 AA.
 AC P23427;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Beta-nerve growth factor precursor (Beta-NGF).
 GN NGFB.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Rattus.
 OC NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89037223; PubMed=3184206;

RA Whitehead S.R., Friedman P.L., Lathammar D.G., Persson H.,
 RA Gonzalez-Carvajal M., Holets V.R.,
 RT "Rat beta-nerve growth factor sequence and site of synthesis in the
 RT adult hippocampus.";
 RL J. Neurosci. Res. 20:403-410(1998).
 RN [2]
 RP SEQUENCE OF 178-219 FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Liver;
 RX MEDLINE=9122573; PubMed=2025430;
 RA Hallboeck F., Ibanez C.F., Persson H.,
 RT "Evolutionary studies of the nerve growth factor family reveal a
 RT novel member abundantly expressed in Xenopus ovary.";
 RL Neuron 6:845-858(1991).
 CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
 CC MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT
 CC STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
 CC EMBRYONIC SENSORY NEURONS.
 CC -1- SUBUNIT: HOMODIMER, ASSOCIATED BY NONCOVALENT FORCES.
 CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
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 CC -----
 DR EMBL; M36589; AAA1697.1; ALT_INIT.
 DR HSBP; P01139; 1BET.
 DR InterPro; IPR002072; NGF.
 DR Pfam; PF00243; NGF; 1.
 DR PRINTS; PR00268; NGF.
 DR ProDom; PD002052; NGF; 1.
 DR SMART; SM00140; NGF; 1.
 DR PROSITE; PS00248; NGF; 1; 1.
 DR PROSITE; PS50270; NGF; 2; 1.
 DR Growth factor; Signal.
 FT SIGNAL 1 18
 FT PROPEP 19 121
 FT CHAIN 122 241
 FT DISULFID 136 201
 FT DISULFID 179 229
 FT DISULFID 189 231
 FT CARBOHYD 69 69
 FT CARBOHYD 114 114
 FT CARBOHYD 166 166
 FT SEQUENCE 241 AA; 27009 MW; 665F42371563213D CRC64;
 SQ
 Query Match 86.9%; Score 1102; DB 1; Length 241;
 Best Local Similarity 85.4%; Pred. No. 3.6e-97;
 Matches 205; Conservative 15; Mismatches 20; Indels 0; Gaps 0;
 Oy 1 MSMLFYTLITLPLGIQAEPPHSESNVPAHGHTIPQVHWTGLQHSIDTALRRASAPAAIA 60
 Db 1 MSMLFYTLITLPLGIQAEPPHSESNVPAHGHTIPQVHWTGLQHSIDTALRRASAPAAIA 60
 Oy 61 ARVAGGTENIVDPLFKKRLRSPRLVPSNOPREAADTQDLDEVGGAAPFSTHRSK 120
 Db 61 ARVAGGTENIVDPLFKKRLRSPRLVPSNOPREAADTQDLDEVGGAAPFSTHRSK 120
 Oy 121 RSSHPHIFRGEFSVCDVSVMVGDKTATDICKERVAVLGEVINNSVFKQYFETCKR 180
 Db 121 RSSHPHIFRGEFSVCDVSVMVGDKTATDICKERVAVLGEVINNSVFKQYFETCKR 180
 Oy 121 RSSHPHIFRGEFSVCDVSVMVGDKTATDICKERVAVLGEVINNSVFKQYFETCKR 180
 Db 121 RSSHPHIFRGEFSVCDVSVMVGDKTATDICKERVAVLGEVINNSVFKQYFETCKR 180
 Oy 181 DPNPDSGCRGIDSGHNSYCTTTTFYKALTMGQKAAAPRIRIDTACVCLSKAVAR 240
 Db 181 DPNPDSGCRGIDSGHNSYCTTTTFYKALTMGQKAAAPRIRIDTACVCLSKAVAR 240
 Oy 181 APNPVSESGCRGIDSGHNSYCTTTTFYKALTMGQKAAAPRIRIDTACVCLSKAVAR 240
 Db 181 APNPVSESGCRGIDSGHNSYCTTTTFYKALTMGQKAAAPRIRIDTACVCLSKAVAR 240
 RESULT 4
 NGF_BOVIN STANDARD; PRT; 231 AA.

AC P13600; O18969;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Beta-nerve growth factor precursor (beta-NGF) (fragment).
 GN NGF.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RX MEDLINE=97430845; PubMed=9284944;
 RA Ridaque C., Laurent P., Hayes H., Rodellar C., Levezuel H.,
 RT "Assignment of the beta-nerve growth factor (NGF) to bovine
 RT chromosome 3 band q23 by in situ hybridization.";
 RL Cytogenet. Cell Genet. 77:306-307(1997).
 RN [2]
 RP SEQUENCE OF 107-231 FROM N.A.
 RX MEDLINE=8630647; PubMed=2427334;
 RA Meier R., Becker-Andre M., Gotz R., Heumann R., Shaw A., Thoenen H.,
 RT "Molecular cloning of bovine and chick nerve growth factor (NGF):
 RT delineation of conserved and unconserved domains and their
 RT relationship to the biological activity and antigenicity of NGF.";
 RL EMBO J. 5:1489-1493(1986).
 CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
 CC MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT
 CC STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
 CC EMBRYONIC SENSORY NEURONS.
 CC -1- SUBUNIT: HOMODIMER, ASSOCIATED BY NONCOVALENT FORCES.
 CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
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 CC -----
 DR EMBL; Y09566; CA970759.1; -
 DR EMBL; M26809; AAA30666.1; -
 DR PIR; A26312; A26312.
 DR HSBP; P01139; 1BET.
 DR InterPro; IPR002072; NGF.
 DR Pfam; PF00243; NGF; 1.
 DR ProDom; PD002052; NGF; 1.
 DR SMART; SM00140; NGF; 1.
 DR PROSITE; PS00248; NGF; 1; 1.
 DR PROSITE; PS50270; NGF; 2; 1.
 DR Growth factor; Signal.
 FT SIGNAL 1 1
 FT NON TER 1
 FT CHAIN 9 111
 FT DISULFID 112 231
 FT DISULFID 126 191
 FT DISULFID 169 219
 FT DISULFID 179 221
 FT CARBOHYD 156 156
 FT CARBOHYD 118 118
 FT CARBOHYD 161 161
 FT CONFLICT 230 231
 FT CONFLICT 231 231
 FT SEQUENCE 231 AA; 25437 MW; 0160509291A418C CRC64;
 SQ
 Query Match 86.8%; Score 1101; DB 1; Length 231;
 Best Local Similarity 90.3%; Pred. No. 4.2e-97;
 Matches 204; Conservative 8; Mismatches 14; Indels 0; Gaps 0;
 Oy 11 AFLLGIQAEPPHSESNVPAHGHTIPQVHWTGLQHSIDTALRRASAPAAIARVAGGTENI 70
 Db 11 AFLLGIQAEPPHSESNVPAHGHTIPQVHWTGLQHSIDTALRRASAPAAIARVAGGTENI 70


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Db 1 MSMLFYLITAFILIGVQAEPTDYNVEDSVEAHMTKLOHSLDTPARRASAPAPIA 60
QY 61 ARVAGOTRNTITVDPRLFKKRLRSFVLPSTQPPREADTODLDFVGAAPSRTRSK 120
Db 61 ARVAGOTRNTITVDPRLFKKRLRSFVLPSTQPPREADTODLDFVGAAPSRTRSK 120
QY 121 RSSHPHIFRGEFSVCDYSVWVGDKTTATDIDKGEVNLGEVNNINSVFQYFEETKCR 180
Db 121 RSSHPHIFRGEFSVCDYSVWVGDKTTATDIDKGEVNLGEVNNINSVFQYFEETKCR 180
QY 121 RSSHPHIFRGEFSVCDYSVWVGDKTTATDIDKGEVNLGEVNNINSVFQYFEETKCR 180
Db 121 RSSHPHIFRGEFSVCDYSVWVGDKTTATDIDKGEVNLGEVNNINSVFQYFEETKCR 180
QY 181 DPNPVDGCGRGIDSGHNSYCTTHTFVKALTMGDKOAMRFIRIDTACVCLSRKAVR 240
Db 181 DPNPVDGCGRGIDSGHNSYCTTHTFVKALTMGDKOAMRFIRIDTACVCLSRKAVR 240
QY 181 DPNPVDGCGRGIDSGHNSYCTTHTFVKALTMGDKOAMRFIRIDTACVCLSRKAVR 240
Db 181 DPNPVDGCGRGIDSGHNSYCTTHTFVKALTMGDKOAMRFIRIDTACVCLSRKAVR 240

RESULT 6
NGF_CAVPO STANDARD; PRT; 241 AA.
ID_NGF_CAVPO
AC P19093;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Beta-nerve growth factor precursor (beta-NGF).
GN NGFB.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriognath; Cavidae; Cavia.
OX NCBI_TaxId=10141;
RN [1]
RS SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RX MEDLINE=89177243; PubMed=2926397;
RA Schwarz M.A., Fisher D., Bradshaw R.A., Isackson P.J.;
RT "Isolation and sequence of a cDNA clone of beta-nerve growth factor
from the guinea pig prostate gland."
RL J. Neurochem. 52:1203-1209(1989).
CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT
STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
EMBRONIC SENSORY NEURONS.
CC -1- SUBUNIT: HOMODIMER, ASSOCIATED BY NONCOVALENT FORCES.
CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
DR HSP: P01139; 1BRT.
DR InterPro: IPR002072; NGF.
DR Pfam: PF00243; NGF.
DR PRINTS: PR00268; NGF.
DR ProDom: PD002052; NGF.
DR SMART: SM00140; NGF.
DR PROSITE: PS00248; NGF_1; 1.
DR PROSITE: PS50270; NGF_2; 1.
KW Growth factor; Signal.
FT SIGNAL 1
FT PROPEP 18
FT CHAIN 122
FT DISULFID 136
FT DISULFID 179
FT DISULFID 189
FT CARBOHYD 69
FT CARBOHYD 114
SQ SEQUENCE 241 AA; 26621 MW; 2F4E26B197804BFA CRC64;

Query Match 85.7%; Score 1087; DB 1; Length 241;
Best Local Similarity 85.8%; Pred. No. 9.4e-96;
Matches 206; Conservative 11; Mismatches 23; Indels 0; Gaps 0;

1 MSMLFYLITAFILIGVQAEPTDYNVEDSVEAHMTKLOHSLDTPARRASAPAPIA 60
1 MSMLFYLITAFILIGVQAEPTDYNVEDSVEAHMTKLOHSLDTPARRASAPAPIA 60
1 ARVAGOTRNTITVDPRLFKKRLRSFVLPSTQPPREADTODLDFVGAAPSRTRSK 120
1 ARVAGOTRNTITVDPRLFKKRLRSFVLPSTQPPREADTODLDFVGAAPSRTRSK 120
1 ARVAGOTRNTITVDPRLFKKRLRSFVLPSTQPPREADTODLDFVGAAPSRTRSK 120

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QY 121 RSSHPHIFRGEFSVCDYSVWVGDKTTATDIDKGEVNLGEVNNINSVFQYFEETKCR 180
Db 121 RSSHPHIFRGEFSVCDYSVWVGDKTTATDIDKGEVNLGEVNNINSVFQYFEETKCR 180
QY 121 RSSHPHIFRGEFSVCDYSVWVGDKTTATDIDKGEVNLGEVNNINSVFQYFEETKCR 180
Db 121 RSSHPHIFRGEFSVCDYSVWVGDKTTATDIDKGEVNLGEVNNINSVFQYFEETKCR 180
QY 181 DPNPVDGCGRGIDSGHNSYCTTHTFVKALTMGDKOAMRFIRIDTACVCLSRKAVR 240
Db 181 DPNPVDGCGRGIDSGHNSYCTTHTFVKALTMGDKOAMRFIRIDTACVCLSRKAVR 240
QY 181 DPNPVDGCGRGIDSGHNSYCTTHTFVKALTMGDKOAMRFIRIDTACVCLSRKAVR 240
Db 181 DPNPVDGCGRGIDSGHNSYCTTHTFVKALTMGDKOAMRFIRIDTACVCLSRKAVR 240

RESULT 7
NGF_PRANA STANDARD; PRT; 241 AA.
ID_NGF_PRANA
AC P20675;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Beta-nerve growth factor precursor (beta-NGF).
GN NGFB.
OS Pracomys natalensis (African soft-furred rat) (Mastomys natalensis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
OC Mastomys.
OX NCBI_TaxId=10112;
RN [1]
RS SEQUENCE FROM N.A.
RX MEDLINE=89172070; PubMed=3234767;
RA Fahnestock M., Bell R.A.;
RT "Molecular cloning of a cDNA encoding the nerve growth factor
precursor from Mastomys natalensis."
RL Gene 69:257-264(1988).
CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT
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EMBRONIC SENSORY NEURONS.
CC -1- SUBUNIT: HOMODIMER, ASSOCIATED BY NONCOVALENT FORCES.
CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
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or send an email to license@ebi.ac.uk.)
CC EMBL; M22748; AAA40599.1; ALT_INIT.
DR PIR; J0343; NGRTA.
DR HSP: P01139; 1BRT.
DR InterPro: IPR002072; NGF.
DR Pfam: PF00243; NGF.
DR PRINTS: PR00268; NGF.
DR ProDom: PD002052; NGF.
DR SMART: SM00140; NGF.
DR PROSITE: PS00248; NGF_1; 1.
DR PROSITE: PS50270; NGF_2; 1.
KW Growth factor; Signal.
FT SIGNAL 1
FT PROPEP 18
FT CHAIN 122
FT DISULFID 136
FT DISULFID 179
FT DISULFID 189
FT CARBOHYD 69
FT CARBOHYD 114
SQ SEQUENCE 241 AA; 27035 MW; 8BFB207A1FEB2F7 CRC64;

Query Match 84.2%; Score 1068; DB 1; Length 241;
Best Local Similarity 82.9%; Pred. No. 5.9e-94;
Matches 199; Conservative 18; Mismatches 23; Indels 0; Gaps 0;

1 MSMLFYLITAFILIGVQAEPTDYNVEDSVEAHMTKLOHSLDTPARRASAPAPIA 60

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Db 1 MSMTFTLLTALLIGVQAEPTDSDNLPBGDSVPEAHMTKQSLDPLARASAPAPIA 60
Qy 61 ARVAGTNRNITVDPRLFKRRRLSPRVLPSTQPPREADTODLDFEVGAAFPSTRSK 120
Db 61 ARVAGTNRNITVDPRLFKRRRLSPRVLPSTQPPREADTODLDFEVGAAFPSTRSK 120
Qy 121 BSSSHPIFRKGEFVSVDVSVVWGDKTTATDICKGEVWVLGEVINNSVFKQYFETKCR 180
Db 121 BSSSHPIFRKGEFVSVDVSVVWGDKTTATDICKGEVWVLGEVINNSVFKQYFETKCR 180
Qy 181 DENPVDGCGRGIDSKHMSYCTTTHFVKALTMDDKQAMRIRIDTACVCLSKAVR 240
Db 181 AANPVBSSGCGIDSKHMSYCTTTHFVKALTMDDKQAMRIRIDTACVCLSKAVR 240

RESULT 8
NGF_CHICK STANDARD; PRT; 243 AA.
AC POS300;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Beta-nerve growth factor precursor (Beta-NGF).
GN NGF.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RX SEQUENCE FROM N.A. MEDLINE=86300646; PubMed=3017695;
RA Eberhard T., Lathimmar D., Persson H.;
RT "Structure and expression of the chicken beta nerve growth factor
gene."
RL EMO J. 5:1483-1487(1986).
RN [2]
RP SEQUENCE OF 118-243 FROM N.A. MEDLINE=86248129; PubMed=3720959;
RA Wilson D., Perret C., Frechin N., Keller A., Behar G., Brachet P.,
RA Auffray C.;
RT "Molecular cloning of the avian beta-nerve growth factor gene:
transcription in brain."
RL PNAS Lett. 203:82-86(1986).
RN [3]
RP SEQUENCE OF 121-243 FROM N.A. MEDLINE=86300647; PubMed=2427334;
RA Meier R., Becker-Andre M., Gotz R., Heumann R., Shaw A., Thoenen H.;
RT "Molecular cloning of bovine and chick nerve growth factor (NGF):
delineation of conserved and unconserved domains and their
relationship to the biological activity and antigenicity of NGF."
RL EMO J. 5:1469-1493(1986).
RN [4]
RP SEQUENCE OF 181-222 FROM N.A. MEDLINE=9122573; PubMed=2025430;
RA Hallboeck F., Ibanez C.F., Persson H.;
RT "Evolutionary studies of the nerve growth factor family reveal a
novel member abundantly expressed in Xenopus ovary."
RL Neuron 6:845-858(1991).
CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT
STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
EMBRIONIC SENSORY NEURONS.
CC -1- SUBUNIT: HOMODIMER, ASSOCIATED BY NONCOVALENT FORCES.
CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
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CC -----
CC EMBL: X04003; CAA27633.1; ALT_INIT.
CC DR EMBL: X04067; CAA27703.1; -.
CC DR EMBL: M26810; AAA48984.1; -.
CC DR PIR: A24857; A24857.
CC DR PIR: A26311; A26311.
CC DR HSSP: P01139; 1BET.
CC DR InterPro: IPR002072; NGF.
CC DR Pfam: PF00243; NGF; 1.
CC DR PRINTS: PR00268; NGF.
CC DR PRODOM: P002052; NGF; 1.
CC DR SMART: SM00140; NGF; 1.
CC DR PROSITE: PS00248; NGF_1; 1.
CC DR PROSITE: PS0270; NGF_2; 1.
CC KM Growth factor; signal.
CC FT SIGNAL 1 22
CC FT PROPEP 23 125 POTENTIAL.
CC FT CHAIN 126 243 BETA-NERVE GROWTH FACTOR.
CC FT DISULFID 139 204 BY SIMILARITY.
CC FT DISULFID 182 232 BY SIMILARITY.
CC FT DISULFID 192 234 BY SIMILARITY.
CC SQ SEQUENCE 243 AA; 27138 MW; 74C306CB2079DA07 CRC64;

Query Match 61.8%; Score 783.5; DB 1; Length 243;
Best Local Similarity 64.5%; Pred. No. 5.2e-67;
Matches 160; Conservative 21; Mismatches 48; Indels 19; Gaps 6;

Qy 1 MSMTFTLLTALLIGVQAEPTDSDNLPBGDSVPEAHMTKQSLDPLARASAPAPIA 56
Db 5 MSMTFTLLTALLIGVQAEPTDSDNLPBGDSVPEAHMTKQSLDPLARASAPAPIA 57
Qy 57 AAIARVA-----GOTNRNITVDPRLFKRRRLSPRVLPSTQPPREADTODLDFEVGAA 111
Db 58 TT-HGRANMPDGDIEDINIMDQNFKKKRRSRVLPSTQPPVSKRGSTGF-LSSAV 115
Qy 112 PFSRTHRSKSSSHPIFRKGEFVSVDVSVVWGDKTTATDICKGEVWVLGEVINNSVFK 171
Db 116 SLNRRTATKRA-TAPVLRHGEFVSVDVSVVWGDKTTATDICKGEVWVLGEVINNSVFK 174
Qy 172 QYFETCRDPNPNPDSGCGRGIDSKHMSYCTTTHFVKALTMDDKQAMRIRIDTACVC 231
Db 175 QYFETCRDPNPNPDSGCGRGIDSKHMSYCTTTHFVKALTMDDKQAMRIRIDTACVC 234
Qy 232 VLSRKAVR 239
Db 235 VLSRKSGR 242

RESULT 9
NGF_XENLA STANDARD; PRT; 231 AA.
ID NGF_XENLA
AC P1617;
DT 01-MAY-1991 (Rel. 18, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Nerve growth factor precursor (NGF).
OS Xenopus laevis (African clawed frog).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
CC Xenopodidae; Xenopus.
CC OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A. MEDLINE=91362944; PubMed=1888511;
RA Carriero F., Campioni M., Cardinali B., Pierandrei-Amaldi P.;
RT "Structure and expression of the nerve growth factor gene in Xenopus
oocytes and embryos."
RL Mol. Reprod. Dev. 29:313-322(1991).
RN [2]
RP SEQUENCE OF 170-211 FROM N.A. T130UE=Liver;
RX MEDLINE=9122573; PubMed=2025430;

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RA Hallboeck F., Ibanez C.F., Persson H.
 RT "Evolutionary studies of the nerve growth factor family reveal a
 RL novel member abundantly expressed in Xenopus ovary".
 CC Neuron 6:845-858(1991).
 CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
 CC MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT
 CC STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
 CC EMBRYONIC SENSORY NEURONS.
 CC -1- SUBUNIT: HOMODIMER, ASSOCIATED BY NONCOVALENT FORCES.
 CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
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 CC EMBL, X55716; CAA39249.1; ALT_INIT.
 CC PIR, S14481; S14481.
 CC HSSP, P01139; 1BET.
 CC InterPro, IPR002072; NGF.
 CC Pfam, PF00243; NGF_1.
 CC PRINTS, PR00268; NGF_1.
 CC ProDom, PD002052; NGF_1.
 CC SMART, SM00140; NGF_1.
 CC PROSITE, PS00248; NGF_1; 1.
 CC PROSITE, PS50270; NGF_2; 1.
 CC Growth factor: Signal.
 CC FT SIGNAL 1 18
 CC FT PROPEP 19 114
 CC FT CHAIN 115 231
 CC FT DISULFID 128 193
 CC FT DISULFID 171 221
 CC FT DISULFID 181 223
 CC FT CARBOHYD 63 63
 CC FT CARBOHYD 107 107
 CC FT CARBOHYD 158 158
 CC FT SEQUENCE 231 AA; 26416 MW; 72A04E7D00B58C5 CRC64;
 SQ
 Query Match 60.6%; Score 768; DB 1; Length 231;
 Best Local Similarity 63.2%; Pred. No. 1.4e-65;
 Matches 153; Conservative 28; Mismatches 41; Indels 20; Gaps 6;
 QY 1 MSMLFYTLITAFILGIGOAEPHSESNVPAQHT-----IP-QVHMTK-LQHSIDTALRRASA 54
 DB 1 MSMLFYTLITLILISVQAPKTDHAPRSSAKSRIPHHHTKSLHNS----- 49
 QY 55 PAAAIARVAGQTRNITVDPRLLFKKRLRSPLVLFSTOPPREADTDLDLFEVGAAPFS 114
 DB 50 -HGKLEAKPEPVFRNVTVDPLFKRKRFRSPRVLFSTPPPLSEDFQLEH-LDEBSLAN 107
 QY 115 RTHSKSSSSHPITFRHGEPSVCDVSVMVGDTTATDIDIKGKENVVLGSEVINNSVFKQYF 174
 DB 108 KTIYAKR-TVHPVLHKGESVCDVSVMVGKTKATDIDIKGKENVVLGSEVINNSVFKQYF 166
 QY 175 PETCRDPNPVDSGCRGIDSKHNSYCTTHTFVKALTMDSKOAAVRIRIDTACVCL 234
 DB 167 PETCRDPKPVSSGCRGIDAKHNSYCTTHTFVVALTMDSKOAAVRIRIDTACVCL 226
 QY 235 RK 236
 DB 227 RK 228
 RESULT 10
 ID NGF_BUNMU STANDARD; PRT; 243 AA.
 AC P34128;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Nerve growth factor precursor (NGF).
 OS Bungarus multicinctus (Many-banded krait).
 CC Bokaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Lepidosaurs; Squamata; Scleroglossa; Serpentes; Colubroidea;
 CC Elapidae; Bungarinae; Bungarus.
 CC NCBI_TaxID=8616;
 CC [1]
 CC RP SEQUENCE FROM N.A.
 CC RC TISSUE=Venom gland;
 CC RX MEDLINE=93192074; PubMed=7916740;
 RA Danse J.M., Garnier J.M.;
 RT "Molecular cloning of a cDNA encoding a nerve growth factor precursor
 RL from the krait, Bungarus multicinctus".
 CC Growth Factors 8:77-86(1993).
 CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
 CC MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT
 CC STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
 CC EMBRYONIC SENSORY NEURONS AS WELL AS BASAL FOREBRAIN CHOLINERGIC
 CC NEURONS IN THE BRAIN.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
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 CC -----
 CC EMBL, S56212; AAB25729.1; -
 CC HSSP, P01139; 1BET.
 CC InterPro, IPR002072; NGF.
 CC Pfam, PF00243; NGF_1.
 CC PRINTS, PR00268; NGF_1.
 CC ProDom, PD002052; NGF_1.
 CC SMART, SM00140; NGF_1.
 CC PROSITE, PS00248; NGF_1; 1.
 CC PROSITE, PS50270; NGF_2; 1.
 CC Growth factor: Signal.
 CC FT SIGNAL 1 18
 CC FT PROPEP 19 125
 CC FT CHAIN 126 243
 CC FT DISULFID 139 204
 CC FT DISULFID 182 232
 CC FT DISULFID 192 234
 CC FT SEQUENCE 243 AA; 27514 MW; E33F64B142179A08 CRC64;
 SQ
 Query Match 53.0%; Score 671.5; DB 1; Length 243;
 Best Local Similarity 56.1%; Pred. No. 2.1e-56;
 Matches 138; Conservative 29; Mismatches 62; Indels 17; Gaps 5;
 QY 1 MSMLFYTLITAFILGIGOAEPHSESNVPAQHT-----HTIQVHMTKLQHSIDTALRRASAPA 56
 DB 1 MSMLFYTLITLILISVQAPKTDHAPRSSAKSRIPHHHTKSLHNS----- 49
 QY 57 AAIARVAGQTRNITVDPRLLFKKRLRSPLVLFSTOPPREADTDLDLFEVGAAP 112
 DB 61 PKSEDDDELGAANITVDPLFKRKRFRSPRVLFSTPPPLSDEGVKLDLE----- 114
 QY 113 FSRTHRS--KSSSHPIFRHGEPSVCDVSVMVGDTTATDIDIKGKENVVLGSEVINNSVF 170
 DB 115 -DTLRNIMANNENHPVNGEHSVCDVSISVMVTKTKATDIDIKGKENVVLGSEVINNSVF 173
 QY 171 KQYFEETCRDPNPVDSGCRGIDSKHNSYCTTHTFVKALTMDSKOAAVRIRIDTACV 230
 DB 174 KQYFEETCRDPNPVDSGCRGIDSKHNSYCTTHTFVVALTMDSKOAAVRIRIDTACV 223
 QY 231 CVLSRK 236
 DB 234 CVLSRK 239

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RESULT 11
NGF_DABRR
ID NGF_DABRR STANDARD; PRT; 117 AA.
AC P30894;
DT 01-JUL-1993 (Rel. 26, Created)
RT 01-JUL-1993 (Rel. 26, Last sequence update)
DB 01-NOV-1997 (Rel. 35, Last annotation update)
DE Nerve growth factor (NGF)
OS Dabola russelli russelli (Russell's viper) (Vipera russelli russelli).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Viperidae; Viperinae; Dabola.
OX NCBI_TaxID=31159;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=93120151; PubMed=1477101;
RA Koyama J.-I., Inoue S., Ikeda K., Hayashi K.;
RT "Purification and amino-acid sequence of a nerve growth factor from
the venom of Vipera russelli russelli";
RL Biochim. Biophys. Acta 1160:287-292(1992).
CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT
STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
EMERSONIC SENSORY NEURONS AS WELL AS BASAL FOREBRAIN CHOLINERGIC
NEURONS IN THE BRAIN.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
DR HSP; P01139; 1BET.
DR InterPro; IPR002072; NGF.
DR Pfam; PF00243; NGF; 1.
DR PRINTS; PR00268; NGF.
DR ProDom; PD002052; NGF; 1.
DR SMART; SM00140; NGF; 1.
DR PROSITE; PS00248; NGF; 1.
DR PROSITE; PS0270; NGF; 2; 1.
KW Glycoprotein; Growth factor.
FT DISULFID 12 77
FT DISULFID 55 105
FT DISULFID 65 107
FT CARBOHYD 21 21
SQ SEQUENCE 117 AA; 13283 MW; A64559C5FEC11F66 CRC64;

Query Match
Best Local Similarity 74.1%; Score 484; DB 1; Length 117;
Matches 83; Conservative 19; Mismatches 10; Indels 0; Gaps 0;

QY 125 HPIFHGEFVCDVSVVGDGKTATDIDKGRVNLGKRVNINSVPKQYFEETKCRDPNP 184
DB 1 HPIFHGEFVCDVSVVWANKTATDIDKGRVNLGKRVNINSVPKQYFEETKCRDPNP 60

QY 185 VDSGGGIDSKMNSYCTTHTFVKALITMDGKQAAWRFIRIDTACVLSRK 236
DB 61 VPSGGGIDAKKMNSTCTTDTFVRLTIRERQASRFIRINTACVLSRK 112

RESULT 12
NGF_XIPMA
ID NGF_XIPMA STANDARD; PRT; 194 AA.
AC P34129;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Nerve growth factor precursor (NGF).
OS Xiphophorus maculatus (Southern platyfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Perciformes; Atherinomorpha;
OC Cyprinodontiformes; Poeciliidae; Xiphophorus.
OX NCBI_TaxID=8083;
RN [1]
RP SEQUENCE FROM N.A.

```

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RX MEDLINE=92333301; PubMed=1629719;
RA Gocz R., Kaulf F., Scharf M.;
RT "Brain-derived neurotrophic factor is more highly conserved in
structure and function than nerve growth factor during vertebrate
evolution";
RL J. Neurochem. 59:432-442(1992).
CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT
STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
EMERSONIC SENSORY NEURONS AS WELL AS BASAL FOREBRAIN CHOLINERGIC
NEURONS IN THE BRAIN.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
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or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X59941; CAA42566.1; -.
DR HSP; P01139; 1BET.
DR InterPro; IPR002072; NGF.
DR Pfam; PF00243; NGF; 1.
DR PRINTS; PR00268; NGF.
DR ProDom; PD002052; NGF; 1.
DR SMART; SM00140; NGF; 1.
DR PROSITE; PS00248; NGF; 1.
DR PROSITE; PS0270; NGF; 2; 1.
KW Growth factor; Signal.
FT SIGNAL 1 30
FT PROPEP 31 79
FT CHAIN 80 194
FT DISULFID 90 155
FT DISULFID 133 183
FT DISULFID 143 185
SQ SEQUENCE 194 AA; 21596 MW; 0369E0FA51147AE CRC64;

Query Match
Best Local Similarity 59.3%; Score 481.5; DB 1; Length 194;
Matches 99; Conservative 14; Mismatches 39; Indels 15; Gaps 3;

QY 71 TVDRLFLKRLRSPRLVSTQPREADTQDLDFEVGAAPFSRHSKSSHPFHR 130
DB 40 TVDRLFLKRLRSPRLVSTQPREADTQDLDFEVGAAPFSRHSKSSHPFHR 84

QY 131 GEFVCDVSVVWGDGKTATDIDKGRVNLGKRVNINSVPKQYFEETKCRDPNPVDSGR 190
DB 85 GEFVCDVSVVWGDGKTATDIDKGRVNLGKRVNINSVPKQYFEETKCRDPNPVDSGR 144

QY 191 GIDSKMNSYCTTHTFVKALITMDGKQAAWRFIRIDTACVLSRK 237
DB 145 GIDSKMNSYCTTHTFVKALITMDGKQAAWRFIRIDTACVLSRK 191

RESULT 13
NT3_HUMAN
ID NT3_HUMAN STANDARD; PRT; 257 AA.
AC P20783;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Neurotrophin-3 precursor (NT-3) (Neurotrophic factor) (HDNF)
DE (Nerve growth factor 2) (NGF-2).
GN NT3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

```

RA MEDLINE=90262727; PubMed=2344409;
 RA Rosenthal A., Goeddel D.V., Nguyen T., Lewis M., Shih A.,
 RA Laramee G.R., Nikolic K., Winalow J.W.;
 RT "Primary structure and biological activity of a novel human
 RT neurotrophic factor.";
 RL Neuron 4:767-773(1990).
 (2)
 RP SEQUENCE FROM N.A.
 RA MEDLINE=91045937; PubMed=2236018;
 RA Jones K.R., Reichardt L.F.;
 RT "Molecular cloning of a human gene that is a member of the nerve
 RT growth factor family.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:8060-8064(1990).
 (3)
 RP SEQUENCE FROM N.A.
 RA MEDLINE=90306351; PubMed=2365067;
 RA Katsuno Y., Yoshimura K., Nakahama K.;
 RT "Cloning and expression of a cDNA encoding a novel human neurotrophic
 RT factor.";
 RL FEBS Lett. 266:187-191(1990).
 (4)
 RP SEQUENCE FROM N.A.
 RA MEDLINE=91365361; PubMed=1889806;
 RA Malsompierre P.C., le Beau M.M., Espinosa R. III, IP N.Y.,
 RA Belluscio L., de la Monte S.M., Squinto S., Furch M.E.,
 RA Yancopoulos G.D.;
 RT "Human and rat brain-derived neurotrophic factor and neurotrophin-3:
 RT gene structures, distributions, and chromosomal localizations.";
 RL Genomics 10:558-568(1991).
 (5)
 RP SEQUENCE OF 194-236 FROM N.A.
 RA TISSUE=Leukocyte;
 RX MEDLINE=9122573; PubMed=2025430;
 RX Hallboeck F., Ibanez C.F., Persson H.;
 RA "Evolutionary studies of the nerve growth factor family reveal a
 RA novel member abundantly expressed in Xenopus ovary.";
 RL Neuron 6:845-858(1991).
 (6)
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
 RA MEDLINE=95217877; PubMed=7703225;
 RA Robinson R.C., Radziejewski C., Stuart D.I., Jones E.Y.;
 RT "Structure of the brain-derived neurotrophic factor/neurotrophin 3
 RT heterodimer.";
 RL Biochemistry 34:4139-4146(1995).
 (7)
 RP VARIANT GLU-76.
 RX MEDLINE=95251647; PubMed=7733919;
 RA Hattori M., Nanko S.;
 RT "Association of neurotrophin-3 gene variant with severe forms of
 RT schizophrenia.";
 RL Biochem. Biophys. Res. Commun. 209:513-518(1995).
 (8)
 RP VARIANT GLU-76.
 RA MEDLINE=96253892; PubMed=8925252;
 RA Aizumi T., Takekoshi K., Itozawa M., Hamaguchi H., Tori M.;
 RT "Failure to find associations of the CA repeat polymorphism in the
 RT first intron and the Gly-63/Glu-63 polymorphism of the neurotrophin-3
 RT gene with schizophrenia.";
 RL Psychiatr. Genet. 6:13-15(1996).
 (9)
 RP FUNCTION: SEEMS TO PROMOTES THE SURVIVAL OF VISCERAL AND
 RP PROPRIOCEPTIVE SENSORY NEURONS.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: BRAIN AND PERIPHERAL TISSUES.
 CC -1- POLYMORPHISM: Variant Glu-76 (frequently reported as Glu-63) was
 CC thought to be associated with severe forms of schizophrenia. This
 CC does not seem to be the case.
 CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
 CC
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 CC -----
 DR EMBL; X53655; CAA37703.1; -;
 DR EMBL; M37763; AAA59953.1; -;
 DR EMBL; M61180; AAA63231.1; -;
 DR PIR; JH0141; JH0141.
 DR PIR; A36208; A36208.
 DR PIR; S10719; S10719.
 DR PIR; C40304; C40304.
 DR PDB; 1BND; 04-APR-96.
 DR PDB; 1B8K; 09-FEB-99.
 DR Genew; HGNC:8023; NTF3.
 DR MIM; 162660; -;
 DR InterPro; IPR002400; GF_cybknot.
 DR InterPro; IPR002072; NGF.
 DR Pfam; PF00243; NGF_1.
 DR PRINTS; PR00438; GFCYSKNOT.
 DR PRINTS; PR00268; NGF.
 DR PRODOM; PD002052; NGF_1.
 DR SMART; SM00140; NGF_1.
 DR PROSITE; PS00248; NGF_1; 1.
 DR PROSITE; PS0270; NGF_2; 1.
 DR Growth factor; Signal; Polymorphism; 3D-structure.
 DR SIGNAL; 1;
 FT PROPEP; 17 138
 FT CHAIN; 139 257 NEUTROPHILIN-3.
 FT DISULFID; 152 217
 FT DISULFID; 195 246
 FT DISULFID; 205 248
 FT CARBOHYD; 131 131
 FT VARIANT; 76 76
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT G->E.
 FT /ftid=VAR_012084.
 SQ SEQUENCE 257 AA; 29354 MW; 39A5B3B28E25E03 CRC64;
 Query Match 37.6%; Score 476.5; DB 1; Length 257;
 Best Local Similarity 40.3%; Pred. No. 6,7e-38;
 Matches 106; Conservative 38; Mismatches 88; Indels 31; Gaps 6;
 QY 1 MSMLFTLTITAFILIGIOAEPSHSNVPAGHTIPQV-----HWTKLOHSLD 45
 DB 1 MSILFYITPLAATLRGIQGNMMDQSLPBDLSNLIITLQADILKNTLSQMWVDKENYO 60
 QY 46 TALRRA-----RSAPAAIAARVAGQTNITVDPRLFK-KERLNSPRVLFSTQPPREA 97
 DB 61 STLPKAPREPREGGAKSAFQPV-----IMADTELLAQGRNYSFRLVLDSTPLER 114
 QY 98 ADYODLDFFVGAAPFSRTSRSSSHPIFRGERSVCDVSVMVGDKTATDINGKEV 157
 DB 115 PPLVIMEDVGSPPVANKTSRRRYAEHK-SHREGYSVCDSESLMTWTDKSAIDIRHQV 173
 QY 158 MVLGEVNIINSVVKQYFEETKCRDPNPVDSGCGGIDSKHNSVCTTHFVRLATMD-GK 216
 DB 174 TVAGEITGNSPVKQYFETRCAPRVKNGCKGIDKHMNSOCKTSQYVRLTSENNK 233
 QY 217 QAARFIRIDYACVYLSSRAVR 239
 DB 234 LVGWRWIRIDTSCVCAISRIGR 256
 RESULT 14
 NT3_XENLA STANDARD; PRT; 260 AA.
 ID NT3_XENLA
 AC P51335;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Neurotrophin-3 precursor (NT-3) (Neurotrophic factor) (HDNF) (Nerve
 DE growth factor 2) (NGF-2).
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.

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OK NCBI_TaxID=8355;
RN SEQUENCE FROM N.A.
RP TISSUE=Brain;
RX MEDLINE=97252639; PubMed=9096131;
RA Xie K., Wang T., Olafsson P., Mizuno K., Lu B.;
RT "Activity-dependent expression of NT-3 in muscle cells in culture:
RL J. Neurosci. 17:2947-2958(1997).
RN SEQUENCE OF 197-217 FROM N.A.
RC TISSUE=Liver; PubMed=2025430;
RX Hallboeck P., Ibanez C.F., Persson H.;
RT "Evolutionary studies of the nerve growth factor family reveal a
RL Neuron 6:845-858(1991).
CC -1- FUNCTION: SEEMS TO PROMOTES THE SURVIVAL OF VISCERAL AND
CC PROPRIOCEPTIVE SENSORY NEURONS.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
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CC -----
DR EMBL; U27576; AAB17723.1; -
DR HSSP; P20783; 1B8K.
DR InterPro; IPRO02400; GF_cysknot.
DR InterPro; IPRO02072; NGF.
DR Pfam; PF00243; NGF; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR PRODOM; PD002052; NGF; 1.
DR SMART; SM00140; NGF; 1.
DR PROSITE; PS00248; NGF_1; 1.
DR PROSITE; PS50270; NGF_2; 1.
DR KMW Growth factor; Signal.
FT SIGNAL 1 16 POTENTIAL.
FT PROPEP 17 141 NEUROTROPHIN-3.
FT CHAIN 142 260 BY SIMILARITY.
FT DISULFID 155 220 BY SIMILARITY.
FT DISULFID 198 249 BY SIMILARITY.
FT DISULFID 208 251 BY SIMILARITY.
FT CARBOHYD 134 134 N-LINKED (GLCNAC... ) (POTENTIAL).
SQ SEQUENCE 260 AA; 30022 MW; FFB8507A5EA93CC5 CRC64;

Query Match 37.0%; Score 469; DB 1; Length 260;
Best Local Similarity 41.2%; Pred. No. 3.5e-37;
Matches 107; Conservative 37; Mismatches 94; Indels 22; Gaps 7;

1 MSMLFYLITLTAFLIGIOAEPRHSESNVPAQH-----TIQVMTK---LQSLDPAKARA 51
||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
1 MSILFYVFLVFLPGICGHATNMKRNLPENSNMSPKLAQALLKKNKSKQVDTKRNHQ 60
||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
52 KAPAPAAIAARVAGQTRN-----ITVDPRLF--KGRILSPRVLFSTQPPREADTQ 101
||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
61 STTPKQQLLDLDGDNDMKQDFQPVLSLAEVLVKQOKQRKRYKSPVLSDSLPLPPPLY 120
||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
102 DLDPEVGGAAPF--STHRSKRSSSHPIFRHGEPSCVDSVWVGDKTTATIDIKGEVWYL 160
||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
121 LMDDYIGHSTVNNNRISRRKRFARHK--GHRGYSVCDSESLVWTIRMAAIDIRGHQVTVL 179
||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
161 GGVNINNSVYKQYFFETKCRDNPVDSGCGIDSKHMNSYCTTHHTPVKALTMQ--GKQAA 219
||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
180 GEIKGNSPVYKQYFETKCRKAPRYVNGCGRIDDKHNSQCTISQTYVALTSNNKAVG 239
||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
220 WAFIRIDTACVCLSKAVR 239
||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

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DB 240 WRWIRIDTSCVCLSKRIGR 259

RESULT 15
NT3_FELCA STANDARD; PRT; 257 AA.
AC 09TSY2;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Neutrotrophin-3 precursor (NT-3) (Neurotrophic factor) (HDNPF)
DE (Nerve growth factor 2) (NGF-2).
GN NT3.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN SEQUENCE FROM N.A.
RP MEDLINE=20211727; PubMed=10745216;
RA Lein E.S., Hohn A., Shatz C.J.;
RT "Dynamic regulation of BDNF and NT-3 expression during visual system
RT development."
J. Comp. Neurol. 420:1-18(2000).
CC -1- FUNCTION: SEEMS TO PROMOTES THE SURVIVAL OF VISCERAL AND
CC PROPRIOCEPTIVE SENSORY NEURONS (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
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CC -----
DR EMBL; AF192538; AAF03424.1; -
DR HSSP; P20783; 1B8K.
DR InterPro; IPRO02072; NGF.
DR Pfam; PF00243; NGF; 1.
DR PRINTS; PR00268; NGF.
DR PRODOM; PD002052; NGF; 1.
DR SMART; SM00140; NGF; 1.
DR PROSITE; PS00248; NGF_1; 1.
DR PROSITE; PS50270; NGF_2; 1.
DR KMW Growth factor; Signal.
FT SIGNAL 1 16 POTENTIAL.
FT PROPEP 17 138 NEUROTROPHIN-3.
FT CHAIN 139 257 BY SIMILARITY.
FT DISULFID 152 217 BY SIMILARITY.
FT DISULFID 195 246 BY SIMILARITY.
FT DISULFID 205 248 BY SIMILARITY.
FT CARBOHYD 131 131 N-LINKED (GLCNAC... ) (POTENTIAL).
SQ SEQUENCE 257 AA; 29403 MW; EB537F85C5113E4 CRC64;

Query Match 36.9%; Score 468.5; DB 1; Length 257;
Best Local Similarity 39.7%; Pred. No. 3.8e-37;
Matches 102; Conservative 41; Mismatches 95; Indels 19; Gaps 5;

1 MSMLFYLITLTAFLIGIOAEPRHSESNVPAQHITPV-----HWTKLQSLD 45
||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
1 MSILFYVFLVFLVLYLNGIGNNNDQSLPDSINSLITKLQADILKKNLSKQWVDLKEYVQ 60
||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
46 TALRRASAPAAIAARVAGQTRNIT--VDPLRFK--KRLRSPRVLFSTQPPREADTQDL 103
||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
61 STLPKAPAPRREDEGEPAKSPFQPVYAMDTELLAQQRKRYKSPVLSDSLPLPPPLYLM 120
||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
104 DFEVGAAPFSGRTHRSKRSSSHPIFRHGEPSCVDSVWVGDKTTATIDIKGEVWYLGEV 163
||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
121 EDVYGSFVAANRTRRRKRYAEHK--SHRGESVLCDSFSLVWTKDSALDIRGHQVTVLGEI 179
||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
164 NINNSVYKQYFFETKCRDNPVDSGCGIDSKHMNSYCTTHHTPVKALTMQ--GKQAAWRF 222
||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

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Db 180 KSGNSPVKQYFETRECKEAPVYNGCRGIDDKHMNSOCTSOYVPAALTSNNKLVGNRW 239
QY 223 IRIDTACVCLSRKAVR 239
Db 240 IRIDTSCVCLSRKIGR 256

Search completed: June 6, 2003, 10:49:55
Job time : 10 secs

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OM protein - protein search, using sw model

Run on: June 6, 2003, 10:49:38 / Search time 17.5 Seconds

(without alignments)
1421.766 Million cell updates/sec

Title: US-09-788-188-2

Perfect score: 1268

Sequence: 1 MSMLFYLITLAFILGIGQAEF.....FIRIDTACCVLSRAAVRRA 241

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 392085 seqs, 103240269 residues

Total number of hits satisfying chosen parameters: 392085

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US08_NEM_PUB pep:*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB pep:*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEM_PUB pep:*
- 4: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB pep:*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB pep:*
- 6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB pep:*
- 7: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB pep:*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB pep:*
- 9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB pep:*
- 10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB pep:*
- 11: /cgn2_6/ptodata/2/pubpaa/US10_NEM_PUB pep:*
- 12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB pep:*
- 13: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB pep:*
- 14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1268	100.0	241	9	US-09-788-188-2
2	1265	99.8	241	9	US-08-450-842-5
3	1265	99.8	241	9	US-09-788-188-1
4	1265	99.8	241	9	US-10-150-262-3
5	1265	99.8	241	9	US-10-155-886-1
6	1265	99.8	241	9	US-10-155-886-6
7	1265	99.8	241	12	US-10-072-681-1
8	1261	99.4	241	9	US-09-822-263-16
9	1244	98.1	241	9	US-10-155-886-7
10	1102	86.9	241	9	US-10-155-886-8
11	1101	86.8	241	9	US-10-155-886-10
12	1091	86.0	241	9	US-10-155-886-9
13	783.5	61.8	243	9	US-10-155-886-11
14	768	60.6	235	9	US-10-155-886-12
15	651	51.3	120	9	US-10-155-886-13
16	651	51.3	120	9	US-10-155-886-14
17	648	51.1	120	9	US-10-155-886-15
18	648	51.1	120	9	US-10-155-886-16
19	647.5	51.1	120	9	US-10-155-886-17
20	647.5	51.1	120	9	US-10-155-886-18

20	642	50.6	153	10	US-09-798-338-2	Sequence 2, Appl
21	642	50.6	163	10	US-09-798-338-6	Sequence 6, Appl
22	621	49.0	121	9	US-09-813-398-9	Sequence 9, Appl
23	614	48.4	121	9	US-10-155-886-33	Sequence 33, Appl
24	602	47.5	120	9	US-10-155-886-35	Sequence 35, Appl
25	584	46.1	118	9	US-10-155-886-40	Sequence 40, Appl
26	584	46.1	120	9	US-10-155-886-38	Sequence 38, Appl
27	584	46.1	121	12	US-10-072-681-3	Sequence 3, Appl
28	566	44.6	117	9	US-10-155-886-42	Sequence 42, Appl
29	507	40.0	121	9	US-10-155-886-37	Sequence 37, Appl
30	500	39.4	125	9	US-10-155-886-35	Sequence 35, Appl
31	479.5	37.8	257	9	US-09-788-188-6	Sequence 6, Appl
32	476.5	37.6	257	8	US-08-450-842-4	Sequence 4, Appl
33	476.5	37.6	257	9	US-09-788-188-5	Sequence 5, Appl
34	476.5	37.6	257	9	US-10-155-886-3	Sequence 3, Appl
35	469	37.0	260	9	US-10-155-886-20	Sequence 20, Appl
36	467	36.8	258	9	US-10-155-886-18	Sequence 18, Appl
37	466.5	36.8	257	9	US-10-155-886-19	Sequence 19, Appl
38	466	36.8	258	9	US-10-155-886-17	Sequence 17, Appl
39	452	35.6	142	8	US-08-450-842-52	Sequence 52, Appl
40	390	30.8	72	10	US-09-848-664-21	Sequence 21, Appl
41	388.5	30.6	119	10	US-09-742-600-6	Sequence 6, Appl
42	388.5	30.6	119	10	US-09-742-600-6	Sequence 6, Appl
43	388.5	30.6	119	10	US-09-742-600-6	Sequence 6, Appl
44	388.5	30.6	120	10	US-09-742-600-3	Sequence 3, Appl
45	388.5	30.6	120	10	US-09-742-600-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-09-788-188-2
Sequence 2, Application US/09788188
Publication No. US20030040082A1
GENERAL INFORMATION:
APPLICANT: BLESCH, MARK
TITLE OF INVENTION: MUTANT PRO-NEUROTROPIN WITH IMPROVED ACTIVITY
FILE REFERENCE: 041673/2045
CURRENT APPLICATION NUMBER: US/09/788, 188
CURRENT FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 241
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Mutant NGF
OTHER INFORMATION: pro-neurotrophin
US-09-788-188-2

Query Match	100.0%	Score 1268	DB 9	Length 241
Best Local Similarity	100.0%	Pred. No. 9.7e-124		
Matches 241	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1	MSMLFYLITLAFILGIGQAEFHSNNPAGHTTIOVMTYLOHSLDPLRRARSAPAAIA 60		
DB	1	MSMLFYLITLAFILGIGQAEFHSNNPAGHTTIOVMTYLOHSLDPLRRARSAPAAIA 60		
QY	61	ARVAGCTRNITVDPRIFKGRRLASPRVLTSTOPPRRAADODDFVGGAAPSRTRRSK 120		
DB	61	ARVAGCTRNITVDPRIFKGRRLASPRVLTSTOPPRRAADODDFVGGAAPSRTRRSK 120		
QY	121	RSSSHPIFRGEFSVCDYSVWVGDKTTATIDIKGEWVYLGENVINNSYFKQYFFETKCR 180		
DB	121	RSSSHPIFRGEFSVCDYSVWVGDKTTATIDIKGEWVYLGENVINNSYFKQYFFETKCR 180		
QY	181	DPNPVDSGGRGIDSKRMNSYCTTHTFVAKLTMDGQAAWRFIRIDTACCVLSRAAVR 240		
DB	181	DPNPVDSGGRGIDSKRMNSYCTTHTFVAKLTMDGQAAWRFIRIDTACCVLSRAAVR 240		

QY 241 A 241
DB 241 A 241

RESULT 2
US-08-450-842-5

/ Sequence 5, Application US/08450842
/ Patent No. US20020045576A1
/ GENERAL INFORMATION:
/ APPLICANT: GENENTECH, INC.
/ APPLICANT: ROSENTHAL, ARNON
/ TITLE OF INVENTION: NOVEL NEUTROPHILIC FACTOR
/ NUMBER OF SEQUENCES: 100
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Genentech, Inc.
/ STREET: 460 Point San Bruno Blvd
/ CITY: South San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94080
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patin (Genentech)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/450,842
/ FILING DATE:
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/426419
/ FILING DATE: 19-APR-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/030013
/ FILING DATE: 23-MAR-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/648482
/ FILING DATE: 31-JAN
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/587707
/ FILING DATE: 1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Torchia, Timothy B.
/ REGISTRATION NUMBER: 36,700
/ REFERENCE/DOCKET NUMBER: 666P2C1D3
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415/225-8674
/ TELEFAX: 415/952-9881
/ TELEX: 910/371-7168
/ INFORMATION FOR SEQ ID NO: 5:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 241 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ US-08-450-842-5

Query Match 99.8%; Score 1265; DB 8; Length 241;
Best Local Similarity 99.6%; Pred. No. 2e-123;

Matches 240; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSMLFTLITAFILGIGIAEPHSESNVPAAGHTIPQVHWTKLOHSLDTALRRARSAPAAIA 60
DB 1 MSMLFTLITAFILGIGIAEPHSESNVPAAGHTIPQVHWTKLOHSLDTALRRARSAPAAIA 60
QY 61 ARVAGQTRNITVDRLFKKRLRSRVLFTSQPREAADTODLDFEVGGAAPFSRTHRSK 120
DB 61 ARVAGQTRNITVDRLFKKRLRSRVLFTSQPREAADTODLDFEVGGAAPFSRTHRSK 120
QY 121 RSSHPITFHGGEFVSCDSVSWVGDKTATDIDIKGEVWVLGEVNIINSVFQYFFETKCR 180
DB 121 RSSHPITFHGGEFVSCDSVSWVGDKTATDIDIKGEVWVLGEVNIINSVFQYFFETKCR 180

QY 181 DPNVDSGCRGIDSKHNSYCTTHTFVKALTMGKQAMRPIRIDTACVCLSRKAVR 240
DB 181 DPNVDSGCRGIDSKHNSYCTTHTFVKALTMGKQAMRPIRIDTACVCLSRKAVR 240
QY 241 A 241
DB 241 A 241

RESULT 3

US-09-788-188-1
/ Sequence 1, Application US/09788188
/ Publication No. US20030040082A1
/ GENERAL INFORMATION:
/ APPLICANT: TUSZYSKI, MARK
/ APPLICANT: BLESCH, ARMIN
/ TITLE OF INVENTION: MUTANT PRO-NEUTROPHILIN WITH IMPROVED ACTIVITY
/ FILE REFERENCE: 041673/2045
/ CURRENT APPLICATION NUMBER: US/09/788,188
/ CURRENT FILING DATE: 2001-02-16
/ NUMBER OF SEQ ID NOS: 16
/ SOFTWARE: Patent In Ver. 2.1
/ SEQ ID NO 1
/ LENGTH: 241
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-09-788-188-1

Query Match 99.8%; Score 1265; DB 9; Length 241;
Best Local Similarity 99.6%; Pred. No. 2e-123;
Matches 240; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSMLFTLITAFILGIGIAEPHSESNVPAAGHTIPQVHWTKLOHSLDTALRRARSAPAAIA 60
DB 1 MSMLFTLITAFILGIGIAEPHSESNVPAAGHTIPQVHWTKLOHSLDTALRRARSAPAAIA 60
QY 61 ARVAGQTRNITVDRLFKKRLRSRVLFTSQPREAADTODLDFEVGGAAPFSRTHRSK 120
DB 61 ARVAGQTRNITVDRLFKKRLRSRVLFTSQPREAADTODLDFEVGGAAPFSRTHRSK 120
QY 121 RSSHPITFHGGEFVSCDSVSWVGDKTATDIDIKGEVWVLGEVNIINSVFQYFFETKCR 180
DB 121 RSSHPITFHGGEFVSCDSVSWVGDKTATDIDIKGEVWVLGEVNIINSVFQYFFETKCR 180
QY 181 DPNVDSGCRGIDSKHNSYCTTHTFVKALTMGKQAMRPIRIDTACVCLSRKAVR 240
DB 181 DPNVDSGCRGIDSKHNSYCTTHTFVKALTMGKQAMRPIRIDTACVCLSRKAVR 240
QY 241 A 241
DB 241 A 241

RESULT 4

US-10-150-262-3
/ Sequence 3, Application US/10150262
/ Publication No. US20030049264A1
/ GENERAL INFORMATION:
/ APPLICANT: FOSTER, KEITH ALAN
/ APPLICANT: DUGGAN, MICHAEL JOHN
/ APPLICANT: SHONE, CLIFFORD CHARLES
/ TITLE OF INVENTION: CLOSTRIDIAL TOXIN DERIVATIVES ABLE TO MODIFY
/ TITLE OF INVENTION: PERIPHERAL
/ TITLE OF INVENTION: SENSOR APPARENT FUNCTIONS
/ FILE REFERENCE: 023223/0104
/ CURRENT APPLICATION NUMBER: US/10/150,262
/ CURRENT FILING DATE: 2002-05-20
/ PRIOR APPLICATION NUMBER: US/09/447,356
/ PRIOR FILING DATE: 1999-11-22
/ PRIOR APPLICATION NUMBER: 08/945,037
/ PRIOR FILING DATE: 1998-01-12
/ PRIOR APPLICATION NUMBER: GB 9508204.6
/ PRIOR FILING DATE: 1995-04-21

NUMBER OF SEQ ID NOS: 11
 SOFTWARE: Patentin Ver. 2.1
 SEQ ID NO 3
 LENGTH: 241
 TYPE: PRT
 ORGANISM: Murine sp.
 US-10-150-262-3

Query Match 99.8%; Score 1265; DB 9; Length 241;
 Best Local Similarity 99.6%; Pred. No. 2e-123;
 Matches 240; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSMLFTTLTFLIGIOAEPHSESNVPAGHTIPQVHTKLQHSIDTALRRASAPAAIA 60
 DB 1 MSMLFTTLTFLIGIOAEPHSESNVPAGHTIPQVHTKLQHSIDTALRRASAPAAIA 60
 QY 61 ARVAGOTRNTITVDPLFKKRLRSPRVLFSTQPPREADTQDLDFEVGGAAPFNRTHSK 120
 DB 61 ARVAGOTRNTITVDPLFKKRLRSPRVLFSTQPPREADTQDLDFEVGGAAPFNRTHSK 120
 QY 121 RSSSHPIFRHGEFSVCDVSVMVGDKTTATDIKGKRWVLGSEVINNSVFKQYFEETKCR 180
 DB 121 RSSSHPIFRHGEFSVCDVSVMVGDKTTATDIKGKRWVLGSEVINNSVFKQYFEETKCR 180
 QY 181 DPNPVDGCGRIGDSKHMNSYCTTHTFPKALTMGKQAAAFRIRIDTACVLSKAVAR 240
 DB 181 DPNPVDGCGRIGDSKHMNSYCTTHTFPKALTMGKQAAAFRIRIDTACVLSKAVAR 240
 QY 241 A 241
 DB 241 A 241

RESULT 5

US-10-155-886-1
 Sequence 1, Application US/10155886
 Publication No. US20030087804A1
 GENERAL INFORMATION:
 APPLICANT: Hemstead, Barbara L.
 APPLICANT: Lee, Ramee
 APPLICANT: Kermant, Kenneth K.
 APPLICANT: Kermant, Pouneh
 TITLE OF INVENTION: High Affinity Ligand For p75 Neurotrophin Receptor
 FILE REFERENCE: 955-21 Sequence No. US20030087804A1. 1-68
 CURRENT APPLICATION NUMBER: US/10/155,886
 CURRENT FILING DATE: 2002-08-05
 NUMBER OF SEQ ID NOS: 68
 SOFTWARE: Patentin version 3.1
 SEQ ID NO 1
 LENGTH: 241
 TYPE: PRT
 ORGANISM: Homo sapien
 US-10-155-886-1

Query Match 99.8%; Score 1265; DB 9; Length 241;
 Best Local Similarity 99.6%; Pred. No. 2e-123;
 Matches 240; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSMLFTTLTFLIGIOAEPHSESNVPAGHTIPQVHTKLQHSIDTALRRASAPAAIA 60
 DB 1 MSMLFTTLTFLIGIOAEPHSESNVPAGHTIPQVHTKLQHSIDTALRRASAPAAIA 60
 QY 61 ARVAGOTRNTITVDPLFKKRLRSPRVLFSTQPPREADTQDLDFEVGGAAPFNRTHSK 120
 DB 61 ARVAGOTRNTITVDPLFKKRLRSPRVLFSTQPPREADTQDLDFEVGGAAPFNRTHSK 120
 QY 121 RSSSHPIFRHGEFSVCDVSVMVGDKTTATDIKGKRWVLGSEVINNSVFKQYFEETKCR 180
 DB 121 RSSSHPIFRHGEFSVCDVSVMVGDKTTATDIKGKRWVLGSEVINNSVFKQYFEETKCR 180
 QY 181 DPNPVDGCGRIGDSKHMNSYCTTHTFPKALTMGKQAAAFRIRIDTACVLSKAVAR 240
 DB 181 DPNPVDGCGRIGDSKHMNSYCTTHTFPKALTMGKQAAAFRIRIDTACVLSKAVAR 240

QY 241 A 241
 DB 241 A 241

RESULT 6

US-10-155-886-6
 Sequence 6, Application US/10155886
 Publication No. US20030087804A1
 GENERAL INFORMATION:
 APPLICANT: Hemstead, Barbara L.
 APPLICANT: Lee, Ramee
 APPLICANT: Kermant, Kenneth K.
 APPLICANT: Kermant, Pouneh
 TITLE OF INVENTION: High Affinity Ligand For p75 Neurotrophin Receptor
 FILE REFERENCE: 955-21 Sequence No. US20030087804A1. 1-68
 CURRENT APPLICATION NUMBER: US/10/155,886
 CURRENT FILING DATE: 2002-08-05
 NUMBER OF SEQ ID NOS: 68
 SOFTWARE: Patentin version 3.1
 SEQ ID NO 6
 LENGTH: 241
 TYPE: PRT
 ORGANISM: Homo sapien
 US-10-155-886-6

Query Match 99.8%; Score 1265; DB 9; Length 241;
 Best Local Similarity 99.6%; Pred. No. 2e-123;
 Matches 240; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSMLFTTLTFLIGIOAEPHSESNVPAGHTIPQVHTKLQHSIDTALRRASAPAAIA 60
 DB 1 MSMLFTTLTFLIGIOAEPHSESNVPAGHTIPQVHTKLQHSIDTALRRASAPAAIA 60
 QY 61 ARVAGOTRNTITVDPLFKKRLRSPRVLFSTQPPREADTQDLDFEVGGAAPFNRTHSK 120
 DB 61 ARVAGOTRNTITVDPLFKKRLRSPRVLFSTQPPREADTQDLDFEVGGAAPFNRTHSK 120
 QY 121 RSSSHPIFRHGEFSVCDVSVMVGDKTTATDIKGKRWVLGSEVINNSVFKQYFEETKCR 180
 DB 121 RSSSHPIFRHGEFSVCDVSVMVGDKTTATDIKGKRWVLGSEVINNSVFKQYFEETKCR 180
 QY 181 DPNPVDGCGRIGDSKHMNSYCTTHTFPKALTMGKQAAAFRIRIDTACVLSKAVAR 240
 DB 181 DPNPVDGCGRIGDSKHMNSYCTTHTFPKALTMGKQAAAFRIRIDTACVLSKAVAR 240
 QY 241 A 241
 DB 241 A 241

RESULT 7

US-10-072-681-1
 Sequence 1, Application US/10072681
 Patent No. US2002013783A1
 GENERAL INFORMATION:
 APPLICANT: Burton, Louis B.
 APPLICANT: Schmelzer, Charles H.
 APPLICANT: Beck, Joanne T.
 TITLE OF INVENTION: PURIFICATION OF NGR
 FILE REFERENCE: GENENT.037C3
 CURRENT APPLICATION NUMBER: US/10/072,681
 CURRENT FILING DATE: 2002-02-08
 PRIOR APPLICATION NUMBER: 60/030838
 PRIOR FILING DATE: 1996-11-15
 PRIOR APPLICATION NUMBER: 60/047855
 PRIOR FILING DATE: 1997-05-29
 PRIOR APPLICATION NUMBER: 08/970865
 PRIOR FILING DATE: 1997-11-14
 PRIOR APPLICATION NUMBER: 09/363573
 PRIOR FILING DATE: 1999-07-29
 PRIOR APPLICATION NUMBER: 09/675,503

PRIOR FILING DATE: 2000-09-29
 NUMBER OF SEQ ID NOS: 6
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 1
 LENGTH: 242
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-072-681-1

Query Match 99.8%; Score 1265; DB 12; Length 242;
 Best Local Similarity 99.6%; Pred. No. 2e-123;
 Matches 240; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSMLFTLLITPAFLIGIOAEPHSESNVPAGHTIPQVHWTKLOHSLDTALRRARSAPAAIA 60
 DB 2 MSMLFTLLITPAFLIGIOAEPHSESNVPAGHTIPQVHWTKLOHSLDTALRRARSAPAAIA 61
 QY 61 ARVAGQTRNITVDRLFKKRLRSPRVLFSTQPPREAADTODLDFEVGGAAPFSTRHSK 120
 DB 62 ARVAGQTRNITVDRLFKKRLRSPRVLFSTQPPREAADTODLDFEVGGAAPFSTRHSK 121
 QY 121 RSSSHPIFRGSEFVSVCDSVSWVGDKTATDIDKKEVWVLGEVININNSVFQYFFETKCR 180
 DB 122 RSSSHPIFRGSEFVSVCDSVSWVGDKTATDIDKKEVWVLGEVININNSVFQYFFETKCR 181
 QY 181 DNPVDSGCRGIDSKHNSYCTTHTFVKALTMGKQAAWFRIRIDTACVLSKAVR 240
 DB 182 DNPVDSGCRGIDSKHNSYCTTHTFVKALTMGKQAAWFRIRIDTACVLSKAVR 241
 QY 241 A 241
 DB 242 A 242

RESULT 8

US-09-822-263-16
 Sequence 16, Application US/09822263
 Patent No. US20020036598A1

GENERAL INFORMATION:
 APPLICANT: Prayaga, Sudhidas
 APPLICANT: Varnet, Corine
 APPLICANT: Shinkets, Richard A
 APPLICANT: Burgess, Catherine
 APPLICANT: Spytek, Kimberly
 APPLICANT: Tchernyev, Velliar T
 TITLE OF INVENTION: No. US0020036598A1 Polynucleotides and Polypeptides Encoded Th
 FILE REFERENCE: 15966-572 CIP1
 CURRENT APPLICATION NUMBER: US/09/822,263
 CURRENT FILING DATE: 2001-06-15

PRIOR FILING DATE: 2000-09-28
 PRIOR FILING DATE: 2000-09-28
 PRIOR FILING DATE: 1999-09-30
 PRIOR FILING DATE: 1999-10-06
 PRIOR FILING DATE: 1999-10-13
 PRIOR FILING DATE: 1999-12-06
 PRIOR FILING DATE: 2000-06-29
 NUMBER OF SEQ ID NOS: 36
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 16
 LENGTH: 241
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-822-263-16

Query Match 99.4%; Score 1261; DB 10; Length 241;
 Best Local Similarity 99.2%; Pred. No. 5.2e-123;
 Matches 239; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSMLFTLLITPAFLIGIOAEPHSESNVPAGHTIPQVHWTKLOHSLDTALRRARSAPAAIA 60
 DB 1 MSMLFTLLITPAFLIGIOAEPHSESNVPAGHTIPQVHWTKLOHSLDTALRRARSAPAAIA 60
 QY 61 ARVAGQTRNITVDRLFKKRLRSPRVLFSTQPPREAADTODLDFEVGGAAPFSTRHSK 120
 DB 61 ARVAGQTRNITVDRLFKKRLRSPRVLFSTQPPREAADTODLDFEVGGAAPFSTRHSK 120
 QY 121 RSSSHPIFRGSEFVSVCDSVSWVGDKTATDIDKKEVWVLGEVININNSVFQYFFETKCR 180
 DB 121 RSSSHPIFRGSEFVSVCDSVSWVGDKTATDIDKKEVWVLGEVININNSVFQYFFETKCR 180
 QY 181 DNPVDSGCRGIDSKHNSYCTTHTFVKALTMGKQAAWFRIRIDTACVLSKAVR 240
 DB 181 DNPVDSGCRGIDSKHNSYCTTHTFVKALTMGKQAAWFRIRIDTACVLSKAVR 240
 QY 241 A 241
 DB 241 A 241

RESULT 9

US-10-155-886-7
 Sequence 7, Application US/10155886
 Publication No. US20030087804A1

GENERAL INFORMATION:
 APPLICANT: Hempstead, Barbara L.
 APPLICANT: Lee, Ramee
 APPLICANT: Teng, Kenneth K.
 APPLICANT: Keramant, Pounch
 TITLE OF INVENTION: High Affinity Ligand For p75 Neurotrophin Receptor
 FILE REFERENCE: 955-21 Sequence No. US20030087804A1. 1-68
 CURRENT APPLICATION NUMBER: US/10/155,886
 CURRENT FILING DATE: 2002-08-05
 NUMBER OF SEQ ID NOS: 68
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 7
 LENGTH: 241
 TYPE: PRT
 ORGANISM: Gorilla gorilla
 US-10-155-886-7

Query Match 98.1%; Score 1244; DB 9; Length 241;
 Best Local Similarity 98.3%; Pred. No. 3e-121;
 Matches 237; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MSMLFTLLITPAFLIGIOAEPHSESNVPAGHTIPQVHWTKLOHSLDTALRRARSAPAAIA 60
 DB 1 MSMLFTLLITPAFLIGIOAEPHSESNVPAGHTIPQVHWTKLOHSLDTALRRARSAPAAIA 60
 QY 61 ARVAGQTRNITVDRLFKKRLRSPRVLFSTQPPREAADTODLDFEVGGAAPFSTRHSK 120
 DB 61 ARVAGQTRNITVDRLFKKRLRSPRVLFSTQPPREAADTODLDFEVGGAAPFSTRHSK 120
 QY 121 RSSSHPIFRGSEFVSVCDSVSWVGDKTATDIDKKEVWVLGEVININNSVFQYFFETKCR 180
 DB 121 RSSSHPIFRGSEFVSVCDSVSWVGDKTATDIDKKEVWVLGEVININNSVFQYFFETKCR 180
 QY 181 DNPVDSGCRGIDSKHNSYCTTHTFVKALTMGKQAAWFRIRIDTACVLSKAVR 240
 DB 181 DNPVDSGCRGIDSKHNSYCTTHTFVKALTMGKQAAWFRIRIDTACVLSKAVR 240
 QY 241 A 241
 DB 241 A 241

RESULT 10

US-10-155-886-8
 Sequence 8, Application US/10155886
 Publication No. US20030087804A1

GENERAL INFORMATION:
 APPLICANT: Hempstead, Barbara L.

APPLICANT: Lee, Ramnee
 APPLICANT: Teng, Kenneth K.
 APPLICANT: Kermani, Pouneh
 TITLE OF INVENTION: High Affinity Ligand For p75 Neurotrophin Receptor
 FILE REFERENCE: 955-21 Sequence No. US20030087804A1. 1-68
 CURRENT APPLICATION NUMBER: US/10/155,886
 NUMBER OF SEQ ID NOS: 68
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 8
 LENGTH: 241
 TYPE: PRT
 ORGANISM: Rattus norvegicus
 US-10-155-886-8

Query Match 86.9%; Score 1102; DB 9; Length 241;
 Best Local Similarity 85.4%; Pred. No. 1,7e-106;
 Matches 205; Conservative 15; Mismatches 20; Indels 0; Gaps 0;

1 MSMLFTLITAFILGIAEPHSESNVPAAGHTIPQVHMTKLOHSLDTALRRASAPAAIA 60
 1 MSMLFTLITAFILGIAEPHSESNVPAAGHTIPQVHMTKLOHSLDTALRRASAPAAIA 60
 61 ARVAGQTRNITVDPRIFKRRRLSPRVLFSTOPPBEADTODLDFEYGAAPSRTRSK 120
 61 ARVAGQTRNITVDPRIFKRRRLSPRVLFSTOPPBEADTODLDFEYGAAPSRTRSK 120
 121 RSSSHPIFRGGEFSVCDVSVMVGDKTATDIDKGEVWVLGEVNINNSVFKQYFFETKCR 180
 121 RSSSHPIFRGGEFSVCDVSVMVGDKTATDIDKGEVWVLGEVNINNSVFKQYFFETKCR 180
 121 RSTHVFHMGFSVCDVSVMVGDKTATDIDKGEVWVLGEVNINNSVFKQYFFETKCR 180
 181 DNPVDSGGRGIDSGKMNSTCTTHTFVKALITMDGKQAMRFIRIDTACVLSKRAVR 240
 181 ARNPVDSGGRGIDSGKMNSTCTTHTFVKALITMDGKQAMRFIRIDTACVLSKRAVR 240

RESULT 11
 US-10-155-886-10

Sequence 10, Application US/10155886
 Publication No. US20030087804A1
 GENERAL INFORMATION:
 APPLICANT: Hempstead, Barbara L.
 APPLICANT: Lee, Ramnee
 APPLICANT: Teng, Kenneth K.
 APPLICANT: Kermani, Pouneh
 TITLE OF INVENTION: High Affinity Ligand For p75 Neurotrophin Receptor
 FILE REFERENCE: 955-21 Sequence No. US20030087804A1. 1-68
 CURRENT APPLICATION NUMBER: US/10/155,886
 NUMBER OF SEQ ID NOS: 68
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 10
 LENGTH: 231
 TYPE: PRT
 ORGANISM: Bos taurus
 US-10-155-886-10

Query Match 86.8%; Score 1101; DB 9; Length 231;
 Best Local Similarity 90.3%; Pred. No. 2.1e-106;
 Matches 204; Conservative 8; Mismatches 14; Indels 0; Gaps 0;

11 AFLIGIOAEPHSESNVPAAGHTIPQVHMTKLOHSLDTALRRASAPAAIAARVAGQTRNI 70
 1 AFLIGIOAEPHSESNVPAAGHTIPQVHMTKLOHSLDTALRRASAPAAIAARVAGQTRNI 70
 71 TVDPRIFKRRRLSPRVLFSTOPPBEADTODLDFEYGAAPSRTRSKSSHPHIFR 130
 71 TVDPRIFKRRRLSPRVLFSTOPPBEADTODLDFEYGAAPSRTRSKSSHPHIFR 130
 61 TVDPRIFKRRRLSPRVLFSTOPPBEADTODLDFEYGAAPSRTRSKSSHPHIFR 120
 131 GEFVCDVSVMVGDKTATDIDKGEVWVLGEVNINNSVFKQYFFETKCRDNPVDSGCR 190
 121 GEFVCDVSVMVGDKTATDIDKGEVWVLGEVNINNSVFKQYFFETKCRDNPVDSGCR 180

191 GIDSKHNSYCTTHTFVKALITMDGKQAMRFIRIDTACVLSRK 226
 181 GIDAKHNSYCTTHTFVKALITMDGKQAMRFIRIDTACVLSRK 226

RESULT 12
 US-10-155-886-9

Sequence 9, Application US/10155886
 Publication No. US20030087804A1
 GENERAL INFORMATION:
 APPLICANT: Hempstead, Barbara L.
 APPLICANT: Lee, Ramnee
 APPLICANT: Teng, Kenneth K.
 APPLICANT: Kermani, Pouneh
 TITLE OF INVENTION: High Affinity Ligand For p75 Neurotrophin Receptor
 FILE REFERENCE: 955-21 Sequence No. US20030087804A1. 1-68
 CURRENT APPLICATION NUMBER: US/10/155,886
 NUMBER OF SEQ ID NOS: 68
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 9
 LENGTH: 241
 TYPE: PRT
 ORGANISM: Mus musculus
 US-10-155-886-9

Query Match 86.0%; Score 1091; DB 9; Length 241;
 Best Local Similarity 84.6%; Pred. No. 2.4e-105;
 Matches 203; Conservative 15; Mismatches 22; Indels 0; Gaps 0;

1 MSMLFTLITAFILGIAEPHSESNVPAAGHTIPQVHMTKLOHSLDTALRRASAPAAIA 60
 1 MSMLFTLITAFILGIAEPHSESNVPAAGHTIPQVHMTKLOHSLDTALRRASAPAAIA 60
 61 ARVAGQTRNITVDPRIFKRRRLSPRVLFSTOPPBEADTODLDFEYGAAPSRTRSK 120
 61 ARVAGQTRNITVDPRIFKRRRLSPRVLFSTOPPBEADTODLDFEYGAAPSRTRSK 120
 121 RSSSHPIFRGGEFSVCDVSVMVGDKTATDIDKGEVWVLGEVNINNSVFKQYFFETKCR 180
 121 RSTHVFHMGFSVCDVSVMVGDKTATDIDKGEVWVLGEVNINNSVFKQYFFETKCR 180
 181 DNPVDSGGRGIDSGKMNSTCTTHTFVKALITMDGKQAMRFIRIDTACVLSKRAVR 240
 181 ASNPVDSGGRGIDSGKMNSTCTTHTFVKALITMDGKQAMRFIRIDTACVLSKRAVR 240

RESULT 13
 US-10-155-886-11

Sequence 11, Application US/10155886
 Publication No. US20030087804A1
 GENERAL INFORMATION:
 APPLICANT: Hempstead, Barbara L.
 APPLICANT: Lee, Ramnee
 APPLICANT: Teng, Kenneth K.
 APPLICANT: Kermani, Pouneh
 TITLE OF INVENTION: High Affinity Ligand For p75 Neurotrophin Receptor
 FILE REFERENCE: 955-21 Sequence No. US20030087804A1. 1-68
 CURRENT APPLICATION NUMBER: US/10/155,886
 NUMBER OF SEQ ID NOS: 68
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 11
 LENGTH: 243
 TYPE: PRT
 ORGANISM: Gallus gallus
 US-10-155-886-11

Query Match 61.8%; Score 783.5; DB 9; Length 243;
 Best Local Similarity 64.5%; Pred. No. 2.2e-73;
 Matches 160; Conservative 21; Mismatches 48; Indels 19; Gaps 6;

1 MSMLFTLITAFILGIAEPHSESN---VPAGHTIPQVHMTKLOHSLDTALRRASAPAA 56

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Db      5 MSMLYTLTLLIAFLITQAPKSEBNDGPLEYPAHSLPSTQSGNH-----AKAAPQ 57
QY      57 AAIARVA-----GGTRNTVDPRLFKRRRLSPVLPTSTOPPREAATODLDEVGGA 111
Db      58 TTHRRFAMPDGTEDLNIAMDONTFKKRRSSSVLSTSTOPPSRKQSGTGF-LSSAV 115
QY      112 PPSRTRSRSSSHPIFHRGEFVSVDVSVWVGDKTTATDIDKGEVWVLGEVNNINSVK 171
Db      116 SLNRTARTKR-TAHPVLRHGEFVSVDVSVWVGDKTTATDIDKGEVWVLGEVNNINSVK 174
QY      172 QYFETKCRDPNPVDSGCGIDSKHNSYCTTHTFVKALTMDSKQAAWRFIRIDTACVC 231
Db      175 QYFETKCRDPNPVDSGCGIDSKHNSYCTTHTFVKALTMDSKQAAWRFIRIDTACVC 234
QY      232 VLSRAVR 239
Db      235 VLSRSGR 242

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RESULT 14

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US-10-155-886-12
; Sequence 12, Application US/10155886
; Publication No. US20030087804A1
; GENERAL INFORMATION:
; APPLICANT: Hempstead, Barbara L.
; APPLICANT: Lee, Ramee
; APPLICANT: Teng, Kenneth K.
; APPLICANT: Kermani, Rouneh
; TITLE OF INVENTION: High Affinity Ligand For p75 Neurotrophin Receptor
; FILE REFERENCE: 955-21 Sequence No. US20030087804A1. 1-68
; CURRENT FILING DATE: 2002-08-05
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Xenopus laevis
US-10-155-886-12

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Query Match      60.6%; Score 768; DB 9; Length 235;
Best Local Similarity 63.2%; Pred. No. 8.6e-72;
Matches 153; Conservative 28; Mismatches 41; Indels 20; Gaps 6;

QY      1 MSMLFYTLITAPLIGIAEPHSESNPAGHT----IP-QVHWTK-LQHSIDTLRRARSA 54
Db      5 MSMLYTLTLLIAFLITQAPKSEBNDGPLEYPAHSLPSTQSGNH-----AKAAPQ 57
QY      55 PAAAIARVAGOTNTITVDPRLFKRRRLSPVLPTSTOPPREAATODLDEVGGAAPS 114
Db      54 -HGKLSAKBPSYFRNTVDPKLFKRRKSPVLPTSTOPPSLSEDPQHLEY-LDDESLN 111
QY      115 RTFRSRSSSHPIFHRGEFVSVDVSVWVGDKTTATDIDKGEVWVLGEVNNINSVK 174
Db      112 KTRIRAGR-TVHPVLRHGEFVSVDVSVWVGDKTTATDIDKGEVWVLGEVNNINSVK 170
QY      175 FETKCRDPNPVDSGCGIDSKHNSYCTTHTFVKALTMDSKQAAWRFIRIDTACVC 234
Db      171 FETKCRDPNPVDSGCGIDSKHNSYCTTHTFVKALTMDSKQAAWRFIRIDTACVC 230
QY      235 RK 236
Db      231 RK 232

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RESULT 15

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US-10-150-262-1
; Sequence 1, Application US/10150262
; Publication No. US20030049264A1
; GENERAL INFORMATION:
; APPLICANT: FOSTER, KEITH ALAN
; APPLICANT: DUGGAN, MICHAEL JOHN

```

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; APPLICANT: SHONE, CLIFFORD CHARLES
; TITLE OF INVENTION: CLOSTRIDIAL TOXIN DERIVATIVES ABLE TO MODIFY
; TITLE OF INVENTION: PERIPHERAL
; FILE REFERENCE: 023223/0104
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: US/10/150,262
; PRIOR FILING DATE: 1999-11-22
; PRIOR APPLICATION NUMBER: 08/945,037
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: GB 9508204.6
; PRIOR FILING DATE: 1995-04-21
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Murine sp.
US-10-150-262-1

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Query Match      51.3%; Score 651; DB 9; Length 120;
Best Local Similarity 100.0%; Pred. No. 4.9e-60;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      122 SSSHPHFHRGEFVSVDVSVWVGDKTTATDIDKGEVWVLGEVNNINSVKQYFETKCRD 161
Db      1 SSSHPHFHRGEFVSVDVSVWVGDKTTATDIDKGEVWVLGEVNNINSVKQYFETKCRD 60
QY      182 PNPVDSGCGIDSKHNSYCTTHTFVKALTMDSKQAAWRFIRIDTACVCVLSRKAVRA 241
Db      61 PNPVDSGCGIDSKHNSYCTTHTFVKALTMDSKQAAWRFIRIDTACVCVLSRKAVRA 120

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Search completed: June 6, 2003, 10:52:46
Job time : 17.5 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: June 6, 2003, 10:48:22 ; Search time 12.5 Seconds
(without alignment)
567.274 Million cell updates/sec

Title: US-09-788-188-2

Perfect score: 1268
Sequence: 1 MSMLFYLITAFILIGIQAE.....FIRIDTACVCLSRKAVRA 241

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
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3: /cgn2_6/prodata/1/aa/5B COMB pep.*
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21: /cgn2_6/prodata/1/aa/6R COMB pep.*
22: /cgn2_6/prodata/1/aa/6S COMB pep.*
23: /cgn2_6/prodata/1/aa/6T COMB pep.*
24: /cgn2_6/prodata/1/aa/6U COMB pep.*
25: /cgn2_6/prodata/1/aa/6V COMB pep.*
26: /cgn2_6/prodata/1/aa/6W COMB pep.*
27: /cgn2_6/prodata/1/aa/6X COMB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1265	99.8	241	1	US-08-266-080B-4
2	1265	99.8	241	1	US-08-451-947-5
3	1265	99.8	241	2	US-08-424-826A-5
4	1265	99.8	241	2	US-08-595-043A-75
5	1265	99.8	241	3	US-08-970-865-1
6	1265	99.8	241	3	US-08-928-694-5
7	1265	99.8	241	4	US-09-363-573-1
8	1265	99.8	241	4	US-09-447-356-3
9	1265	99.8	241	5	PCT-US91-06950-5
10	1265	99.8	241	5	PCT-US95-05423-4
11	1265	99.8	242	4	US-09-675-503-1
12	1265	99.8	240	3	US-08-910-691-11
13	1265	99.8	240	1	US-08-440-049-3
14	1265	99.8	240	3	US-08-441-513A-3
15	1265	99.8	240	3	US-08-581-663-31
16	1265	99.8	240	4	US-08-845-541B-1
17	1265	99.8	240	4	US-09-066-065A-1
18	1265	99.8	240	4	US-09-447-356-1
19	1265	99.8	240	4	US-09-664-295-31
20	1265	99.8	240	5	PCT-US95-06918-3
21	1265	99.8	240	3	US-08-970-865-2
22	1265	99.8	240	4	US-09-363-573-2
23	1265	99.8	240	4	US-09-675-503-2
24	1265	99.8	240	4	US-09-675-922-4
25	1265	99.8	240	4	US-09-675-922-8
26	1265	99.8	240	3	US-08-753-642-2
27	1265	99.8	240	4	US-09-675-922-2

28	642	50.6	163	4	US-09-675-922-6	Sequence 6, Appl
29	637	50.2	120	4	US-08-845-541B-3	Sequence 3, Appl
30	637	50.2	120	4	US-09-066-065A-3	Sequence 3, Appl
31	634	50.0	120	4	US-08-845-541B-4	Sequence 4, Appl
32	634	50.0	120	4	US-09-066-065A-4	Sequence 4, Appl
33	629	49.6	120	4	US-08-845-541B-12	Sequence 12, Appl
34	629	49.6	120	4	US-09-066-065A-12	Sequence 12, Appl
35	628	49.5	120	4	US-08-845-541B-17	Sequence 17, Appl
36	628	49.5	120	4	US-08-845-541B-20	Sequence 20, Appl
37	628	49.5	120	4	US-09-066-065A-17	Sequence 17, Appl
38	628	49.5	120	4	US-08-845-541B-18	Sequence 18, Appl
39	626	49.4	120	4	US-08-845-541B-21	Sequence 21, Appl
40	626	49.4	120	4	US-09-066-065A-18	Sequence 18, Appl
41	626	49.4	120	4	US-09-066-065A-21	Sequence 21, Appl
42	623	49.1	120	4	US-08-845-541B-13	Sequence 13, Appl
43	623	49.1	120	4	US-08-845-541B-19	Sequence 19, Appl
44	623	49.1	120	4	US-09-066-065A-13	Sequence 13, Appl
45	623	49.1	120	4	US-09-066-065A-13	Sequence 13, Appl

ALIGNMENTS

RESULT 1
US-08-266-080B-4
Sequence 4, Application US/08266080B
Patent No. 5606031
GENERAL INFORMATION:
APPLICANT: Jack Lile
APPLICANT: Tadahiko Kohno
APPLICANT: Duane Bonam
TITLE OF INVENTION: Production of Biologically Active
NUMBER OF INVENTION: Recombinant Neurotrophic Protein
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSER: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/266,080B
FILING DATE: 27-JUNE-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/240,122
FILING DATE: 09-MAY-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/087,912
FILING DATE: 06-JULY-1993
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/680,681
FILING DATE: 04-APRIL-1991
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/594,126
FILING DATE: 09-OCT-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/547,750
FILING DATE: 02-JULY-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/505,441
FILING DATE: 06-APRIL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: SYNE200C5
TELECOMMUNICATION INFORMATION:

TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 241 amino acids
TYPE: amino acid
TOPOLOGY: linear
FEATURE:
NAME/KEY: inferred amino acid sequence of human NGF
US-08-266-0808-4

Query Match 99.8%; Score 1265; DB 1; Length 241;
Best Local Similarity 99.6%; Pred. No. 7.1e-142;
Matches 240; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSMLFYTLITAFILGIAEPHSESNVPAGHTIPQVHTKLOHSIDTLRRASAPAAIA 60
DB 1 MSMLFYTLITAFILGIAEPHSESNVPAGHTIPQVHTKLOHSIDTLRRASAPAAIA 60
QY 61 ARVAGOTRNTITVDPRLFKKRLSPRLPSTOPPREADTDODLDFEVGGAAPFRTSKR 120
DB 61 ARVAGOTRNTITVDPRLFKKRLSPRLPSTOPPREADTDODLDFEVGGAAPFRTSKR 120
QY 121 RSSSHPIFRHGEFSVCDVSVMGDKTTATDIDKKEVMVLGEVINNSVFKQYFFETKCR 180
DB 121 RSSSHPIFRHGEFSVCDVSVMGDKTTATDIDKKEVMVLGEVINNSVFKQYFFETKCR 180
QY 181 DPNPVDSCGCRGIDSKHNSYCTTHTFYKALTMGKQAMRFIRIDTACVCLSRKAVR 240
DB 181 DPNPVDSCGCRGIDSKHNSYCTTHTFYKALTMGKQAMRFIRIDTACVCLSRKAVR 240
QY 241 A 241
DB 241 A 241

RESULT 2

US-08-451-947-5
Sequence 5, Application US/08451947

Patent No. 5702906
GENERAL INFORMATION:
APPLICANT: GENE TECH, INC.
APPLICANT: ROSENTHAL, ARNON
TITLE OF INVENTION: NOVEL NEUROTROPHIC FACTOR
NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/451.947
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/426419
FILING DATE: 19-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/030013
FILING DATE: 22-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/648482
FILING DATE: 31-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/587707
FILING DATE: 1991

ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: 666P2CID2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-8674
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 241 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-451-947-5

Query Match 99.8%; Score 1265; DB 1; Length 241;
Best Local Similarity 99.6%; Pred. No. 7.1e-142;
Matches 240; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSMLFYTLITAFILGIAEPHSESNVPAGHTIPQVHTKLOHSIDTLRRASAPAAIA 60
DB 1 MSMLFYTLITAFILGIAEPHSESNVPAGHTIPQVHTKLOHSIDTLRRASAPAAIA 60
QY 61 ARVAGOTRNTITVDPRLFKKRLSPRLPSTOPPREADTDODLDFEVGGAAPFRTSKR 120
DB 61 ARVAGOTRNTITVDPRLFKKRLSPRLPSTOPPREADTDODLDFEVGGAAPFRTSKR 120
QY 121 RSSSHPIFRHGEFSVCDVSVMGDKTTATDIDKKEVMVLGEVINNSVFKQYFFETKCR 180
DB 121 RSSSHPIFRHGEFSVCDVSVMGDKTTATDIDKKEVMVLGEVINNSVFKQYFFETKCR 180
QY 181 DPNPVDSCGCRGIDSKHNSYCTTHTFYKALTMGKQAMRFIRIDTACVCLSRKAVR 240
DB 181 DPNPVDSCGCRGIDSKHNSYCTTHTFYKALTMGKQAMRFIRIDTACVCLSRKAVR 240
QY 241 A 241
DB 241 A 241

RESULT 3

US-08-424-826A-5
Sequence 5, Application US/08424826A

Patent No. 5830858
GENERAL INFORMATION:
APPLICANT: Rosenthal, Arnon
APPLICANT: ROSENTHAL, ARNON
TITLE OF INVENTION: NOVEL NEUROTROPHIC FACTOR
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/424.826A
FILING DATE: 19-APR-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/240387
FILING DATE: 10-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/648482
FILING DATE: 31-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/587707
FILING DATE: 25-SEP-1990

ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Phd., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P0666P1C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-8674
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 241 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-424-826A-5

Query Match 99.8%; Score 1265; DB 2; Length 241;
Best Local Similarity 99.6%; Pred. No. 7,1e-142;
Matches 240; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSMLFYTLITFLIGIOAEPHSESNVPAAGTTPQVHTKLOHSIDTLARRASAPAAIA 60
DB 1 MSMLFYTLITFLIGIOAEPHSESNVPAAGTTPQVHTKLOHSIDTLARRASAPAAIA 60
QY 61 ARVAGQTRNITVDRLFRKRLRSPRVLFSTQPREAADTODLFEVGAAPFSTTRSK 120
DB 61 ARVAGQTRNITVDRLFRKRLRSPRVLFSTQPREAADTODLFEVGAAPFSTTRSK 120
QY 121 RSSHPIFHGEFVCDVSVWVGDKTTATDIDKKEVMVLGEVNNINSVFQYFFETKCR 180
DB 121 RSSHPIFHGEFVCDVSVWVGDKTTATDIDKKEVMVLGEVNNINSVFQYFFETKCR 180
QY 181 DPNFVDSGCRGIDSKHNSYCTTHTFVKALTMGQAAVRFIRIDTACVLSKAVRR 240
DB 181 DPNFVDSGCRGIDSKHNSYCTTHTFVKALTMGQAAVRFIRIDTACVLSKAVRR 240
QY 241 A 241
DB 241 A 241

RESULT 4

US-08-595-043A-75
Sequence 75, Application US/08595043A
Patent No. 5935824
GENERAL INFORMATION:
APPLICANT: SGARLATO, GREGORY D.
TITLE OF INVENTION: PROTEIN EXPRESSION SYSTEM
NUMBER OF SEQUENCES: 90
CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL
STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/595,043A
FILING DATE: 31-JAN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: SGAR-00371
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 75:
SEQUENCE CHARACTERISTICS:

LENGTH: 241 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-595-043A-75

Query Match 99.8%; Score 1265; DB 2; Length 241;
Best Local Similarity 99.6%; Pred. No. 7,1e-142;
Matches 240; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSMLFYTLITFLIGIOAEPHSESNVPAAGTTPQVHTKLOHSIDTLARRASAPAAIA 60
DB 1 MSMLFYTLITFLIGIOAEPHSESNVPAAGTTPQVHTKLOHSIDTLARRASAPAAIA 60
QY 61 ARVAGQTRNITVDRLFRKRLRSPRVLFSTQPREAADTODLFEVGAAPFSTTRSK 120
DB 61 ARVAGQTRNITVDRLFRKRLRSPRVLFSTQPREAADTODLFEVGAAPFSTTRSK 120
QY 121 RSSHPIFHGEFVCDVSVWVGDKTTATDIDKKEVMVLGEVNNINSVFQYFFETKCR 180
DB 121 RSSHPIFHGEFVCDVSVWVGDKTTATDIDKKEVMVLGEVNNINSVFQYFFETKCR 180
QY 181 DPNFVDSGCRGIDSKHNSYCTTHTFVKALTMGQAAVRFIRIDTACVLSKAVRR 240
DB 181 DPNFVDSGCRGIDSKHNSYCTTHTFVKALTMGQAAVRFIRIDTACVLSKAVRR 240
QY 241 A 241
DB 241 A 241

RESULT 5

US-08-970-865-1
Sequence 1, Application US/08970865
Patent No. 6005081
GENERAL INFORMATION:
APPLICANT: Louis E. Burton, Charles H. Schmelzer, Joanne T. Beck
TITLE OF INVENTION: Purification of NGF
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94060
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/970,865
FILING DATE: 14-NOV-1997
CLASSIFICATION: 530
APPLICATION NUMBER: 60/030838
FILING DATE: 11/15/1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/047855
FILING DATE: 5/29/1997
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Phd., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1063R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 241 amino acids
TYPE: Amino Acid
TOPOLOGY: linear

US-08-970-865-1

Query Match 99.8%; Score 1265; DB 3; Length 241;
Best Local Similarity 99.6%; Pred. No. 7.1e-142;
Matches 240; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSMLFYTLITAFILGIAOBPHSESNVPAGHTIPQVHWTKLOHSLDTALRRASAPAAATA 60
DB 1 MSMLFYTLITAFILGIAOBPHSESNVPAGHTIPQVHWTKLOHSLDTALRRASAPAAATA 60
QY 61 ARVAGQTRNITVDPRLPFKKRLRSRVLFTSTOPPREADTODLDPEVGAAPFNRTHSK 120
DB 61 ARVAGQTRNITVDPRLPFKKRLRSRVLFTSTOPPREADTODLDPEVGAAPFNRTHSK 120
QY 121 RSSSHPIFRHGFESVCDVSVMGDKTTATDICKKEVWLGEVNNINSVFKQYFFETKCR 180
DB 121 RSSSHPIFRHGFESVCDVSVMGDKTTATDICKKEVWLGEVNNINSVFKQYFFETKCR 180
QY 181 DPNPVDSCGRGIDSKMNSYCTTHTFVKALTMGKQAAWRFIRIDTACVLSKRAVR 240
DB 181 DPNPVDSCGRGIDSKMNSYCTTHTFVKALTMGKQAAWRFIRIDTACVLSKRAVR 240
QY 241 A 241
DB 241 A 241

RESULT 6

US-08-928-694-5
Sequence 5, Application US/08928694
Patent No. 6037320

GENERAL INFORMATION:

APPLICANT: ROSENTHAL, ARNON
TITLE OF INVENTION: NOVEL NEUROTROPHIC FACTOR
NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/928,694
FILING DATE: 12-Sep-1997

CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/451947
FILING DATE: 26-MAY-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/426419
FILING DATE: 19-APR-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/030013
FILING DATE: 22-MAR-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/648482
FILING DATE: 31-JAN

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/587707
FILING DATE: 1993

ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Ph.D., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P0666P2C1D2C1

TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:
LENGTH: 241 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear

US-08-928-694-5

Query Match 99.8%; Score 1265; DB 3; Length 241;
Best Local Similarity 99.6%; Pred. No. 7.1e-142;
Matches 240; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSMLFYTLITAFILGIAOBPHSESNVPAGHTIPQVHWTKLOHSLDTALRRASAPAAATA 60
DB 1 MSMLFYTLITAFILGIAOBPHSESNVPAGHTIPQVHWTKLOHSLDTALRRASAPAAATA 60
QY 61 ARVAGQTRNITVDPRLPFKKRLRSRVLFTSTOPPREADTODLDPEVGAAPFNRTHSK 120
DB 61 ARVAGQTRNITVDPRLPFKKRLRSRVLFTSTOPPREADTODLDPEVGAAPFNRTHSK 120
QY 121 RSSSHPIFRHGFESVCDVSVMGDKTTATDICKKEVWLGEVNNINSVFKQYFFETKCR 180
DB 121 RSSSHPIFRHGFESVCDVSVMGDKTTATDICKKEVWLGEVNNINSVFKQYFFETKCR 180
QY 181 DPNPVDSCGRGIDSKMNSYCTTHTFVKALTMGKQAAWRFIRIDTACVLSKRAVR 240
DB 181 DPNPVDSCGRGIDSKMNSYCTTHTFVKALTMGKQAAWRFIRIDTACVLSKRAVR 240
QY 241 A 241
DB 241 A 241

RESULT 7

US-09-363-573-1
Sequence 1, Application US/09363573
Patent No. 6184360

GENERAL INFORMATION:

APPLICANT: Louis E. Burton, Charles H. Schmeizer, Joanne T. Beck
TITLE OF INVENTION: Purification of NGR
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/363,573
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/970,865
FILING DATE: 5/29/1997

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/047855
FILING DATE: 5/29/1997

ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Ph.D., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1063R2

TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
LENGTH: 241 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear

LENGTH: 241 amino acids
 TYPE: Amino Acid
 TOPOLOGY: Linear
 US-09-363-573-1

Query Match 99.8%; Score 1265; DB 4; Length 241;

Best Local Similarity 99.6%; Pred. No. 7.1e-142;
 Matches 240; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSMLFTLLTFLAFLIGIOAEPHSESVPAGHTIPQVHMTKLOHSLDTPALRRASAPAAIA 60
 DB 1 MSMLFTLLTFLAFLIGIOAEPHSESVPAGHTIPQVHMTKLOHSLDTPALRRASAPAAIA 60
 QY 61 ARVAGOTRNTITVDPRLFKKRLRSPPVLFSTOPPREADTODLDFEVGAAPFNRTTHRSK 120
 DB 61 ARVAGOTRNTITVDPRLFKKRLRSPPVLFSTOPPREADTODLDFEVGAAPFNRTTHRSK 120
 QY 121 RSSSHPIFRHGEFSVCDVSVMGDKTTATDIKGKXVWVLGEVNNINSVFKQYFFETKCR 180
 DB 121 RSSSHPIFRHGEFSVCDVSVMGDKTTATDIKGKXVWVLGEVNNINSVFKQYFFETKCR 180
 QY 181 DPNPVDGCGRGIDSKHNSYCTTHTTFVKALTMGKQAAAFIRIDTACVCLSRKAVR 240
 DB 181 DPNPVDGCGRGIDSKHNSYCTTHTTFVKALTMGKQAAAFIRIDTACVCLSRKAVR 240
 QY 241 A 241
 DB 241 A 241

RESULT 8

US-09-447-356-3

Sequence 3, Application US/09447356
 Patent No. 639513

GENERAL INFORMATION:
 APPLICANT: FOSTER, KEITH ALAN
 APPLICANT: DUGAN, MICHAEL JOHN
 APPLICANT: SHONE, CLIFFORD CHARLES
 TITLE OF INVENTION: CLOSTRIDIUM TOXIN DERIVATIVES ABLE TO MODIFY PERIPHERAL
 TITLE OF INVENTION: SENSORY AFFERENT FUNCTIONS
 FILE REFERENCE: 023223/0104
 CURRENT APPLICATION NUMBER: US/09/447,356
 PRIOR FILING DATE: 1999-11-22
 PRIOR APPLICATION NUMBER: 08/945,037
 PRIOR FILING DATE: 1998-01-12
 PRIOR APPLICATION NUMBER: GB 9508204.6
 PRIOR FILING DATE: 1995-04-21
 NUMBER OF SEQ ID NOS: 11
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 3
 LENGTH: 241
 TYPE: PRT
 ORGANISM: Murine sp.
 US-09-447-356-3

Query Match 99.8%; Score 1265; DB 4; Length 241;

Best Local Similarity 99.6%; Pred. No. 7.1e-142;
 Matches 240; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSMLFTLLTFLAFLIGIOAEPHSESVPAGHTIPQVHMTKLOHSLDTPALRRASAPAAIA 60
 DB 1 MSMLFTLLTFLAFLIGIOAEPHSESVPAGHTIPQVHMTKLOHSLDTPALRRASAPAAIA 60
 QY 61 ARVAGOTRNTITVDPRLFKKRLRSPPVLFSTOPPREADTODLDFEVGAAPFNRTTHRSK 120
 DB 61 ARVAGOTRNTITVDPRLFKKRLRSPPVLFSTOPPREADTODLDFEVGAAPFNRTTHRSK 120
 QY 121 RSSSHPIFRHGEFSVCDVSVMGDKTTATDIKGKXVWVLGEVNNINSVFKQYFFETKCR 180
 DB 121 RSSSHPIFRHGEFSVCDVSVMGDKTTATDIKGKXVWVLGEVNNINSVFKQYFFETKCR 180
 QY 181 DPNPVDGCGRGIDSKHNSYCTTHTTFVKALTMGKQAAAFIRIDTACVCLSRKAVR 240
 DB 181 DPNPVDGCGRGIDSKHNSYCTTHTTFVKALTMGKQAAAFIRIDTACVCLSRKAVR 240

DB 181 DPNPVDGCGRGIDSKHNSYCTTHTTFVKALTMGKQAAAFIRIDTACVCLSRKAVR 240
 QY 241 A 241
 DB 241 A 241

RESULT 9

PCT-US91-06950-5

Sequence 5, Application PC/TUS9106950
 GENERAL INFORMATION:

APPLICANT: GENENTECH, INC.
 APPLICANT: ROSENTHAL, ARNON
 TITLE OF INVENTION: NOVEL NEUTROTROPHIC FACTOR
 NUMBER OF SEQUENCES: 100
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 460 Point San Bruno Blvd
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: patin (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US91/06950
 FILING DATE: 19910924
 CLASSIFICATION: 436
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/648482
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/587707
 ATTORNEY/AGENT INFORMATION:
 NAME: Hensley, Max D.
 REGISTRATION NUMBER: 27,043
 REFERENCE/DOCKET NUMBER: 666P1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415/266-1994
 TELEFAX: 415/952-9881
 TELEX: 910/371-7168
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 241 amino acids
 TYPE: AMINO ACID
 TOPOLOGY: linear
 PCT-US91-06950-5

Query Match 99.8%; Score 1265; DB 5; Length 241;

Best Local Similarity 99.6%; Pred. No. 7.1e-142;
 Matches 240; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSMLFTLLTFLAFLIGIOAEPHSESVPAGHTIPQVHMTKLOHSLDTPALRRASAPAAIA 60
 DB 1 MSMLFTLLTFLAFLIGIOAEPHSESVPAGHTIPQVHMTKLOHSLDTPALRRASAPAAIA 60
 QY 61 ARVAGOTRNTITVDPRLFKKRLRSPPVLFSTOPPREADTODLDFEVGAAPFNRTTHRSK 120
 DB 61 ARVAGOTRNTITVDPRLFKKRLRSPPVLFSTOPPREADTODLDFEVGAAPFNRTTHRSK 120
 QY 121 RSSSHPIFRHGEFSVCDVSVMGDKTTATDIKGKXVWVLGEVNNINSVFKQYFFETKCR 180
 DB 121 RSSSHPIFRHGEFSVCDVSVMGDKTTATDIKGKXVWVLGEVNNINSVFKQYFFETKCR 180
 QY 181 DPNPVDGCGRGIDSKHNSYCTTHTTFVKALTMGKQAAAFIRIDTACVCLSRKAVR 240
 DB 181 DPNPVDGCGRGIDSKHNSYCTTHTTFVKALTMGKQAAAFIRIDTACVCLSRKAVR 240
 QY 241 A 241
 DB 241 A 241

RESULT 10
PCT-US95-05423-4
Sequence 4, Application PC/TUS9505423
GENERAL INFORMATION:
APPLICANT: Jack Lile
APPLICANT: Tadahiko Kohno
APPLICANT: Duane Bonam
TITLE OF INVENTION: Production of Biologically Active
TITLE OF INVENTION: Recombinant Neurotrophic Protein
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05423
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/266,090
FILING DATE: 27-JUNE-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/240,122
FILING DATE: 09-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/087,912
FILING DATE: 06-JULY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/680,681
FILING DATE: 04-APRIL-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/594,126
FILING DATE: 09-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/547,750
FILING DATE: 02-JULY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/505,441
FILING DATE: 06-APRIL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: SYNE200/PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 241 amino acids
TYPE: amino acid
TOPOLOGY: linear
FEATURE:
NAME/KEY: inferred amino acid sequence of human NGF
PCT-US95-05423-4
Query Match 99.8%; Score 1265; DB 5; Length 241;
Best Local Similarity 99.6%; Pred. No. 7,1e-142;
Matches 240; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSMLFTLITAFILIGIOAEPHSBSNVPAHTIPQVHTKLOHSLDTRARASAPAAIA 60
Db 1 MSMLFTLITAFILIGIOAEPHSBSNVPAHTIPQVHTKLOHSLDTRARASAPAAIA 60

QY 61 ARVAGOTRNTITVDPRLFKKRLRSRVLFTSTQPREADTODLDFEVGAAPFERTRSK 120
Db 61 ARVAGOTRNTITVDPRLFKKRLRSRVLFTSTQPREADTODLDFEVGAAPFERTRSK 120
QY 121 RSSSHPIFRHGEFSCVSVWVGDKTTATDIDKEVWVGEVINNSVFOYFEETKCR 180
Db 121 RSSSHPIFRHGEFSCVSVWVGDKTTATDIDKEVWVGEVINNSVFOYFEETKCR 180
QY 181 DPNPVDGCGRGIDSKHNSYCTTHTFVKALTMGDKQAAVFRIDTACVLSRAVVR 240
Db 181 DPNPVDGCGRGIDSKHNSYCTTHTFVKALTMGDKQAAVFRIDTACVLSRAVVR 240
QY 241 A 241
Db 241 A 241

RESULT 11
US-09-675-503-1
Sequence 1, Application US/09675503
Patent No. 6423831
GENERAL INFORMATION:
APPLICANT: Burton, Louis E.
APPLICANT: Schmelzer, Charles H.
APPLICANT: Beck, Joanne T.
TITLE OF INVENTION: ISOLATION OF NEUROTROPHINS FROM A
TITLE OF INVENTION: MIXTURE CONTAINING OTHER PROTEINS AND NEUROTROPHIN VARIANTS
FILE REFERENCE: GENE 037C2
CURRENT APPLICATION NUMBER: US/09/675,503
CURRENT FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: 60/030838
PRIOR FILING DATE: 1996-11-15
PRIOR APPLICATION NUMBER: 60/047855
PRIOR FILING DATE: 1997-05-29
PRIOR APPLICATION NUMBER: 08/970865
PRIOR FILING DATE: 1997-11-14
PRIOR APPLICATION NUMBER: 09/363573
PRIOR FILING DATE: 1999-07-29
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 242
TYPE: PRT
ORGANISM: Homo sapien
US-09-675-503-1

Query Match 99.8%; Score 1265; DB 4; Length 242;
Best Local Similarity 99.6%; Pred. No. 7,2e-142;
Matches 240; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSMLFTLITAFILIGIOAEPHSBSNVPAHTIPQVHTKLOHSLDTRARASAPAAIA 60
Db 2 MSMLFTLITAFILIGIOAEPHSBSNVPAHTIPQVHTKLOHSLDTRARASAPAAIA 61
QY 61 ARVAGOTRNTITVDPRLFKKRLRSRVLFTSTQPREADTODLDFEVGAAPFERTRSK 120
Db 62 ARVAGOTRNTITVDPRLFKKRLRSRVLFTSTQPREADTODLDFEVGAAPFERTRSK 121
QY 121 RSSSHPIFRHGEFSCVSVWVGDKTTATDIDKEVWVGEVINNSVFOYFEETKCR 180
Db 122 RSSSHPIFRHGEFSCVSVWVGDKTTATDIDKEVWVGEVINNSVFOYFEETKCR 181
QY 181 DPNPVDGCGRGIDSKHNSYCTTHTFVKALTMGDKQAAVFRIDTACVLSRAVVR 240
Db 182 DPNPVDGCGRGIDSKHNSYCTTHTFVKALTMGDKQAAVFRIDTACVLSRAVVR 241
QY 241 A 241
Db 242 A 242

RESULT 12

US-08-910-691-11
Sequence 11, Application US/08910691
Patent No. 6015552
GENERAL INFORMATION:
APPLICANT: MATSUDA, Tatsuya
APPLICANT: YOSHITOMI, Sumie
APPLICANT: SASADA, Reiko
TITLE OF INVENTION: THERAPEUTIC AGENT FOR NEUTROPENIA
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN, DIKE, BRONSTEIN, ROBERTS &
ADDRESS: CUSHMAN
STREET: 130 Water Street
CITY: Boston
STATE: Massachusetts
COUNTRY: US
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/910,691
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/074,969
FILING DATE: 19930604
ATTORNEY/AGENT INFORMATION:
NAME: NEUMER, George W
REGISTRATION NUMBER: 26964
REFERENCE/DOCKET NUMBER: 12345
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)523-3400
TELEFAX: (617)523-6440
TELEX: 200291 STRR UR
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 240 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-910-691-11

Query Match
Best Local Similarity 78.8%; Score 991; DB 3; Length 240;
Matches 189; Conservative 20; Mismatches 29; Indels 2; Gaps 2;

Db
1 MSMLFYLLITFLIGIQAPHSSESVNPAAGHTIPGVHMTKLOHSIDTALRRASAPAAIA 60
1 MSMLFYLLITFLIGIQAPHSSESVNPAAGHTIPGVHMTKLOHSIDTALRRASAPAAIA 60

Qy
61 ARVAGQFRNITVDRLPKRRRLSPRVLFSTQPREADTDLDPEVGAAPFRTSRK 120
61 ARVAGQFRNITVDRLPKRRRLSPRVLFSTQPREADTDLDPEVGAAPFRTSRK 120

Db
121 RSSHPIFHRGSPVCSVWVGDKTTATDIKKEVAVLGEVAINNSVFKQYFEETKCR 180
121 RSSHPIFHRGSPVCSVWVGDKTTATDIKKEVAVLGEVAINNSVFKQYFEETKCR 180

Qy
121 RYAEHR-SHGEISVCSSESLMTDKSALDIRHQVTVLGEITGNSPVQYFEETRCK 179
121 RYAEHR-SHGEISVCSSESLMTDKSALDIRHQVTVLGEITGNSPVQYFEETRCK 179

Db
181 DPNPVDGCGRIDSKHNSYCTTHTFVKALTMQ-GKQAMRFIRIDTACVLSRKAVR 239
181 DPNPVDGCGRIDSKHNSYCTTHTFVKALTMQ-GKQAMRFIRIDTACVLSRKAVR 239

Qy
180 EAPFVKNGCGIDDKHNSQCTTQVRLALTSNNMLVGKRWIRIDTSVCVALSRKIGR 239
180 EAPFVKNGCGIDDKHNSQCTTQVRLALTSNNMLVGKRWIRIDTSVCVALSRKIGR 239

RESULT 13
US-08-440-049-3
Sequence 3, Application US/08440049
Patent No. 5728803
GENERAL INFORMATION:
APPLICANT: Ulfert, Roman
APPLICANT: Preetla, Leonard G.

APPLICANT: Winslow, John W.
TITLE OF INVENTION: PANTROPIC NEUTROTROPHIC FACTORS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,049
FILING DATE: 12-May-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/253937
FILING DATE: 03-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Timothy R.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P0905C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-8674
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-440-049-3

Query Match
Best Local Similarity 51.3%; Score 651; DB 1; Length 120;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy
122 SSSHPIFHRGSPVCSVWVGDKTTATDIKKEVAVLGEVAINNSVFKQYFEETKCRD 181
122 SSSHPIFHRGSPVCSVWVGDKTTATDIKKEVAVLGEVAINNSVFKQYFEETKCRD 181

Db
1 SSSHPIFHRGSPVCSVWVGDKTTATDIKKEVAVLGEVAINNSVFKQYFEETKCRD 60
1 SSSHPIFHRGSPVCSVWVGDKTTATDIKKEVAVLGEVAINNSVFKQYFEETKCRD 60

Qy
182 PNPVDSGCGRIDSKHNSYCTTHTFVKALTMQKQAMRFIRIDTACVLSRKAVRA 241
182 PNPVDSGCGRIDSKHNSYCTTHTFVKALTMQKQAMRFIRIDTACVLSRKAVRA 241

Db
61 PNPVDSGCGRIDSKHNSYCTTHTFVKALTMQKQAMRFIRIDTACVLSRKAVRA 120
61 PNPVDSGCGRIDSKHNSYCTTHTFVKALTMQKQAMRFIRIDTACVLSRKAVRA 120

RESULT 14
US-08-441-513A-3
Sequence 3, Application US/08441513A
Patent No. 5961480
GENERAL INFORMATION:
APPLICANT: Ulfert, Roman
APPLICANT: Preetla, Leonard G.
APPLICANT: Winslow, John W.
TITLE OF INVENTION: Pantropic Neurotrophic Factors
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/441,513A
FILING DATE: 15-May-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/253937
FILING DATE: 03-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Phd., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P0905C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-441-513A-3

Query Match 51.3%; Score 651; DB 3; Length 120;
Best Local Similarity 100.0%; Pred. No. 1.7e-69;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 122 SSSHPFHRGERSVCDVSVMVGDKTATDINGKEMVLGEVNNINSVFKQYFFETKCRD 181
DB 1 SSSHPFHRGERSVCDVSVMVGDKTATDINGKEMVLGEVNNINSVFKQYFFETKCRD 60
QY 182 PNPVDSGCRGIDSKMNSYCTTHTFYKALTMGKQAAWRFIRIDTACVCLSRKAVRRA 241
DB 61 PNPVDSGCRGIDSKMNSYCTTHTFYKALTMGKQAAWRFIRIDTACVCLSRKAVRRA 120

RESULT 15

US-08-581-662-31
Sequence 31, Application US/08581662
Patent No. 6121235
GENERAL INFORMATION:
APPLICANT: Gao, Wei-Qiang
TITLE OF INVENTION: Treatment of Balance Impairments
FILE REFERENCE: P0981
CURRENT APPLICATION NUMBER: US/08/581,662
CURRENT FILING DATE: 1995-12-29
NUMBER OF SEQ ID NOS: 36
SEQ ID NO 31
LENGTH: 120
TYPE: PRT
ORGANISM: Homo sapiens
US-08-581-662-31

Query Match 51.3%; Score 651; DB 3; Length 120;
Best Local Similarity 100.0%; Pred. No. 1.7e-69;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 122 SSSHPFHRGERSVCDVSVMVGDKTATDINGKEMVLGEVNNINSVFKQYFFETKCRD 181
DB 1 SSSHPFHRGERSVCDVSVMVGDKTATDINGKEMVLGEVNNINSVFKQYFFETKCRD 60
QY 182 PNPVDSGCRGIDSKMNSYCTTHTFYKALTMGKQAAWRFIRIDTACVCLSRKAVRRA 241
DB 61 PNPVDSGCRGIDSKMNSYCTTHTFYKALTMGKQAAWRFIRIDTACVCLSRKAVRRA 120

Search completed: June 6, 2003, 10:52:05
Job time: 13.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 6, 2003, 10:46:22 ; Search time 32.5 Seconds
(without alignments)
988.105 Million cell updates/sec

Title: US-09-788-188-2

Perfect score: 1268
Sequence: 1 MSMLFYTLITAFLLIGIQAP.....FIRIDTACVTLSHKAVRA 241

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

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22: /SID52/gcgdata/geneSeq/geneSeq-emb1/AA2001.DAT.*
23: /SID52/gcgdata/geneSeq/geneSeq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1265	99.8	241	12	AA13063 Human NGF Smat-Apa
2	1265	99.8	241	12	AA11474 Human nerve growth
3	1265	99.8	241	12	AA11358 Human nerve growth
4	1265	99.8	241	16	AA17419 Human nerve growth
5	1265	99.8	241	16	AA16688 Human nerve growth
6	1265	99.8	241	18	AA26237 Human preproNGF
7	1265	99.8	241	18	AA14886 Human prepro-nerve
8	1265	99.8	241	20	AA107303 Human NGF. Homo s
9	1265	99.8	241	22	AA166929 Human NGF. Homo s
10	1265	99.8	241	23	AA118904 Human beta nerve g

11	1265	99.8	241	23	AB04994
12	1265	99.8	245	5	AA14038
13	1262	99.5	307	14	AA15241
14	1261	99.4	241	22	AA16785
15	1261	99.4	307	14	AA13799
16	1259	99.3	307	19	AA169725
17	1233	97.2	239	14	AA143910
18	1233	97.2	241	12	AA13886
19	1170	92.3	222	21	AA10884
20	1091	86.0	240	23	AA150845
21	1091	86.0	307	5	AA14036
22	1091	86.0	307	5	AA14039
23	1088	85.8	307	14	AA15240
24	991	78.2	240	15	AA13937
25	991	78.2	240	15	AA156451
26	986	77.8	240	13	AA126273
27	682	53.8	129	14	AA137539
28	682	53.8	129	18	AA124145
29	661	52.1	124	13	AA121851
30	657.5	51.9	154	13	AA122751
31	651	51.3	120	20	AA181117
32	651	51.3	120	21	AA129141
33	651	51.3	120	22	AA164994
34	651	51.3	120	22	AA135944
35	648	51.1	156	23	AA150303
36	648	51.1	157	21	AA101596
37	648	51.1	157	22	AA167677
38	648	51.1	157	23	AA108525
39	647.5	51.1	166	23	AA150301
40	647.5	51.1	167	22	AA167679
41	647	51.0	261	10	AA191299
42	647	51.0	262	7	AA151033
43	643	50.7	120	17	AA190531
44	642	50.6	118	10	AA191034
45	642	50.6	119	5	AA140040

ALIGNMENTS

RESULT 1	AA13063
ID	AA13063 standard; Protein; 241 AA.
AC	AA13063;
XX	
DT	30-SEP-1991 (first entry)
XX	
DE	Human NGF Smat-Apai fragment prod.
XX	
KW	Expression vector; human nerve growth factor; yeast;
KW	benile dementia.
XX	
OS	Homo sapiens.
XX	
PN	JP03139285-A.
XX	
PD	13-JUN-1991.
XX	
PP	20-DEC-1989; 89JP-0328199.
XX	
PR	27-JUL-1989; 89JP-0192581.
XX	
PA	(TAKE) TAKEDA CHEMICAL IND KK.
XX	
DR	WPI: 1991-218449/30.
XX	
DR	N-PSDB; AA012638.
XX	
PT	New yeast expression vector - used in prodn. of human nerve growth
XX	
PT	factor from corresp. yeast.
XX	
PS	Disclosure; Fig 1(1-2); 14pp; Japanese.
XX	

Human beta nerve g
Sequence encoded b
Human pre-pro nerv
Amino acid sequenc
Human NGF. Homo s
Human beta-nerve g
Nerve growth facto
NGF with pro-regio
Human proNGF prote
Mouse nerve growth
Sequence encoded b
Sequence encoded b
Cloned mouse pre-p
Sequence of pro re
Human NGF-2/NT-3 e
NGF2/NT-3 in pTB13
Recombinant beta-N
Chimeric neurotrop
Human growth hormo
Nerve growth facto
N-terminal of neut
Nerve growth facto
NGF-beta amino aci
Nerve growth facto
Nerve growth facto
Amino acid sequenc
Synthetic nerve gr
Nerve growth facto
Amino acid sequenc
Human nerve growth
Human beta-nerve g
Pantropic neurotro
Human nerve growth
Sequence encoded b

CC Human NGF is useful as a reagent for study of the nervous system, and
 CC for treatment of senile dementia. The DNA encoding this fragment was
 CC derived from the human gene or is synthesised chemically.
 CC See also AAQ12639.
 XX
 SQ Sequence 241 AA;

Query Match 99.8%; Score 1265; DB 12; Length 241;
 Best Local Similarity 99.6%; Pred. No. 1.6e-133;
 Matches 240; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSMLFYLITAFILGIGIAEPHSESNVPAGHTIPQVHTKLOHSIDTLARRASAPAAIA 60
 DB 1 MSMLFYLITAFILGIGIAEPHSESNVPAGHTIPQVHTKLOHSIDTLARRASAPAAIA 60
 QY 61 ARVAGOTRNTITVDPRLFKKRLRSFVLFSTQPREAADTODLDFEVGGAAPFRTTRSK 120
 DB 61 ARVAGOTRNTITVDPRLFKKRLRSFVLFSTQPREAADTODLDFEVGGAAPFRTTRSK 120
 QY 121 RSSSHPIFHRGERSVCDVSVMVGDKTTATDINGKKEVMVLGEVNIINSVFQYFFETKCR 180
 DB 121 RSSSHPIFHRGERSVCDVSVMVGDKTTATDINGKKEVMVLGEVNIINSVFQYFFETKCR 180
 QY 181 DENPVDGCGRGIDSKHNSYCTTHTFVKALTMGKQAAFRIRIDTACVCLSRKAVRR 240
 DB 181 DENPVDGCGRGIDSKHNSYCTTHTFVKALTMGKQAAFRIRIDTACVCLSRKAVRR 240
 QY 241 A 241
 DB 241 A 241

RESULT 2
 AAR11474
 ID AAR11474 standard; Protein; 241 AA.

AC AAR11474;
 DT 26-APR-1991 (first entry)
 XX
 DE Human nerve growth factor.
 KW NGF; senile dementia.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..18
 FT Protein /label= signal sequence
 FT Protein /label= pro-NGF
 FT Protein /label= mature NGF
 FT Disulfide-bond 135..202
 FT Disulfide-bond 180..230
 FT Disulfide-bond 190..232
 XX
 PN EP41451-A.
 PD 27-FEB-1991.
 XX
 PR 17-AUG-1990; 90EP-0115815.
 XX
 PR 21-AUG-1989; 89JP-0212980.
 PR 20-DEC-1989; 89JP-0328198.
 PR 13-APR-1990; 90JP-0096252.
 PR 07-JUN-1990; 90JP-0147352.
 XX
 PA (TAKE) TAKEDA CHEMICALS IND KK.
 XX Kakinuma A, Nakahama K, Yoshimura K, Katsubo Y, Iwano M,
 XX WPT, 1991-059398/09.

DR N-PsDB; AAQ10620.
 XX
 PT Human nerve growth factor containing cysteine residues - used as
 PT reagent and therapeutic drug for senile dementia.
 XX
 PS Claim 1; Fig 1; 33pp; English.

The sequence was deduced from a clone isolated from a lambda EMBL3
 CC genomic library prepd. from human leukocyte DNA, using a probe [A.
 CC synthesized based on the sequence of the known human NGF gene [A.
 CC Ullrich et al., Nature 303, 821 (1983)]. The clone, betaLN2113,
 CC isolated from the library was cleaved with SmaI and ApaI to remove
 CC a 1kb fragment contg. the gene which was then inserted into plasmid
 CC pBluescript IIX to obtain pNGFP107G. The gene was sequenced from
 CC this plasmid using SeeDease (Biochemical). The sequence of the
 CC protein coding region was found to be in complete agreement with
 CC that of Ullrich et al. The sequence was used to produce
 CC recombinant h-NGF for use in the prodn. of drugs for e.g. senile
 CC dementia.

Sequence 241 AA;

Query Match 99.8%; Score 1265; DB 12; Length 241;
 Best Local Similarity 99.6%; Pred. No. 1.6e-133;
 Matches 240; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSMLFYLITAFILGIGIAEPHSESNVPAGHTIPQVHTKLOHSIDTLARRASAPAAIA 60
 DB 1 MSMLFYLITAFILGIGIAEPHSESNVPAGHTIPQVHTKLOHSIDTLARRASAPAAIA 60
 QY 61 ARVAGOTRNTITVDPRLFKKRLRSFVLFSTQPREAADTODLDFEVGGAAPFRTTRSK 120
 DB 61 ARVAGOTRNTITVDPRLFKKRLRSFVLFSTQPREAADTODLDFEVGGAAPFRTTRSK 120
 QY 121 RSSSHPIFHRGERSVCDVSVMVGDKTTATDINGKKEVMVLGEVNIINSVFQYFFETKCR 180
 DB 121 RSSSHPIFHRGERSVCDVSVMVGDKTTATDINGKKEVMVLGEVNIINSVFQYFFETKCR 180
 QY 181 DENPVDGCGRGIDSKHNSYCTTHTFVKALTMGKQAAFRIRIDTACVCLSRKAVRR 240
 DB 181 DENPVDGCGRGIDSKHNSYCTTHTFVKALTMGKQAAFRIRIDTACVCLSRKAVRR 240
 QY 241 A 241
 DB 241 A 241

RESULT 3
 AAR13858
 ID AAR13858 standard; Protein; 241 AA.

AC AAR13858;
 DT 21-NOV-1991 (first entry)
 XX
 DE Human nerve growth factor.
 KW hNGF.
 OS Homo sapiens.
 XX
 PN JP03175976-A.
 PD 31-UTL-1991.
 XX
 PR 12-DEC-1989; 89JP-0320483.
 XX
 PR 30-SEP-1989; 89JP-0253796.
 PR 15-DEC-1988; 88JP-0314860.
 PR 12-DEC-1989; 89JP-0320483.
 XX
 PA (TAKE) TAKEDA CHEMICAL IND KK.

DR WPI: 1991-269694/37.
 DR N-PSDB; AAQ13397.
 XX
 PT Secretory prepn. of animal protein - by culturing
 PT Schizosaccharomyces pombe which retains DNA at 3'-terminal of
 PT promoter region.
 XX
 PS Disclosure; Fig 3; 12pp; Japanese.
 CC
 CC The amino acid sequence is encoded that of human nerve growth factor
 CC (NGF). It may be expressed in Schizosaccharomyces pombe using the
 CC glyceraldehyde-3-phosphate dehydrogenase (GHD) gene promoter.
 XX
 SQ Sequence 241 AA;
 Query Match 99.8%; Score 1265; DB 12; Length 241;
 Best Local Similarity 99.6%; Pred. No. 1.6e-133;
 Matches 240; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSMLFYTLITAFLLGLOAEPSHESNVPAAGHTIPQVHTKLOHSIDTLARRASAPAAIA 60
 DB 1 MSMLFYTLITAFLLGLOAEPSHESNVPAAGHTIPQVHTKLOHSIDTLARRASAPAAIA 60
 QY 61 ARVAGQTRNITVDRLFKKRLRSRVLFSSTOPREAADTODLDFEVGAAPFSRTHRSK 120
 DB 61 ARVAGQTRNITVDRLFKKRLRSRVLFSSTOPREAADTODLDFEVGAAPFSRTHRSK 120
 QY 121 RSSSHPIFHRGSEVCSVSVMVGDKTTATDIKGEVMVLGEVININNSVFKQYFFETKCR 180
 DB 121 RSSSHPIFHRGSEVCSVSVMVGDKTTATDIKGEVMVLGEVININNSVFKQYFFETKCR 180
 QY 181 DPNPVDGCGRIDSKHNSYCTTHTFVKALTMGKQAMRFIRIDPACVLSRKAVRR 240
 DB 181 DPNPVDGCGRIDSKHNSYCTTHTFVKALTMGKQAMRFIRIDPACVLSRKAVRR 240
 QY 241 A 241
 DB 241 A 241
 Db
 QY 241 A 241
 DB 241 A 241
 RESULT 4
 AAR77419
 ID AAR77419 standard; Protein; 241 AA.
 AC AAR77419;
 DT 10-FEB-1996 (first entry)
 DE Human nerve growth factor.
 XX
 XX Nerve growth factor; neurotrophic factor; therapeutic;
 XX protein refolding; NGF.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Protein 122..241
 FT /note= "mature protein"
 FT Region 1..121
 FT /note= "pre-region"
 XX
 PN MO9530686-A1.
 XX
 PD 16-NOV-1995.
 XX
 PP 02-MAY-1995; 95MO-US05423.
 PR 27-JUN-1994; 94US-0266080.
 PR 09-MAY-1994; 94US-0240122.
 XX
 PA (SYNT) SYNTAX-SYNERGEN NEUROSCIENCE JOINT VENTU.
 XX
 PI Bonam D, Kohno T, Lile J, Rosendahl MS;

XX
 DR WPI: 1995-404080/51.
 DR N-PSDB; AAT05437.
 XX
 PT Process for bacterial expression of recombinant neurotrophic factor
 PT - useful for promoting the survival and maintaining phenotypic
 PT differentiation of nerve and glial cells.
 XX
 PS Disclosure; Page 33-34; 57pp; English.
 CC
 CC The nerve growth factor (NGF) gene is expressed in *Bacterichia*
 CC *coli* cells. The recombinant protein is solubilized and
 CC sulfonlated and allowed to refold in the presence of PEG and urea.
 CC Biologically active NGF, used for promoting the survival of and
 CC maintaining the phenotypic differentiation of nerve and glial cells,
 CC is isolated and purified. This method breaks incorrectly formed
 CC disulphide bonds and allows refolding of the factor into the correct
 CC tertiary structure required for maximum yield of full active protein.
 XX
 SQ Sequence 241 AA;
 Query Match 99.8%; Score 1265; DB 16; Length 241;
 Best Local Similarity 99.6%; Pred. No. 1.6e-133;
 Matches 240; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSMLFYTLITAFLLGLOAEPSHESNVPAAGHTIPQVHTKLOHSIDTLARRASAPAAIA 60
 DB 1 MSMLFYTLITAFLLGLOAEPSHESNVPAAGHTIPQVHTKLOHSIDTLARRASAPAAIA 60
 QY 61 ARVAGQTRNITVDRLFKKRLRSRVLFSSTOPREAADTODLDFEVGAAPFSRTHRSK 120
 DB 61 ARVAGQTRNITVDRLFKKRLRSRVLFSSTOPREAADTODLDFEVGAAPFSRTHRSK 120
 QY 121 RSSSHPIFHRGSEVCSVSVMVGDKTTATDIKGEVMVLGEVININNSVFKQYFFETKCR 180
 DB 121 RSSSHPIFHRGSEVCSVSVMVGDKTTATDIKGEVMVLGEVININNSVFKQYFFETKCR 180
 QY 181 DPNPVDGCGRIDSKHNSYCTTHTFVKALTMGKQAMRFIRIDPACVLSRKAVRR 240
 DB 181 DPNPVDGCGRIDSKHNSYCTTHTFVKALTMGKQAMRFIRIDPACVLSRKAVRR 240
 QY 241 A 241
 DB 241 A 241
 Db
 QY 241 A 241
 DB 241 A 241
 RESULT 5
 AAR66688
 ID AAR66688 standard; Protein; 241 AA.
 AC AAR66688;
 DT 23-AUG-1995 (first entry)
 DE Human nerve growth factor.
 XX
 XX Human nerve growth factor; hNGF; polyclonal antibody;
 XX immunogen; enzyme immunoassay.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..18
 FT /label= sig_peptide
 FT Peptide 19..121
 FT /label= pro_peptide
 FT Misc-difference 8
 FT /note= "corresponding codon TCG"
 FT Misc-difference 59
 FT /note= "corresponding codon TAT"
 FT Misc-difference 173
 FT /note= "corresponding codon TAG"
 FT Disulfide-bond 136..201

FT Disulfide-bond 179..229
FT Disulfide-bond 189..231
XX JP06317587-A.
XX
XX 15-NOV-1994.
XX
XX 14-FEB-1991, 91JP-0021181.
XX
XX 31-AUG-1990, 90JP-0231317.
XX
XX (TAKE) TAKEDA CHEM IND LTD.
XX
XX WPI: 1995-033116/05.
XX N-PSDB; AAQ79871.
XX
XX Polyclonal antibody against human nerve growth factor (NGF) -
XX useful to detect human NGF, for diagnosis of disease
XX
XX Example 1; Pages 31-33; 35pp; Japanese.
XX
XX AAQ79871 encodes AAR6688 human nerve growth factor (hNGF), the
XX protein was used as an immunogen to generate a polyclonal
XX antibody against hNGF. The polyclonal antibody can be used
XX to detect and determine hNGF pref. by enzyme immunoassay.
XX
SQ Sequence 241 AA;
Query Match 99.8%; Score 1265; DB 16; Length 241;
Best Local Similarity 99.6%; Pred. No. 1.6e-133;
Matches 240; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSMLFTLTITAFILGIAEPHSESNVPAAGHTIPQVHWTKLOHSIDTLARRARSAAPAIA 60
DB 1 MSMLFTLTITAFILGIAEPHSESNVPAAGHTIPQVHWTKLOHSIDTLARRARSAAPAIA 60
QY 61 ARVAGQTRNITVDPLPFKKRLRSPRYLFTSTOPPRAADTQDLDPEVGAAPFNRTRRSK 120
DB 61 ARVAGQTRNITVDPLPFKKRLRSPRYLFTSTOPPRAADTQDLDPEVGAAPFNRTRRSK 120
QY 121 RSSSHPIFRHGEPSVCDVSVMWGDXTATDIDKGEVMVLGEVINNSVFQYFEETKCR 180
DB 121 RSSSHPIFRHGEPSVCDVSVMWGDXTATDIDKGEVMVLGEVINNSVFQYFEETKCR 180
QY 181 DPNPVDGCGRIDSKKMNSTCTTHTFVKALTMDSKQAAWRFIRIDTACVLSRKAARR 240
DB 181 DPNPVDGCGRIDSKKMNSTCTTHTFVKALTMDSKQAAWRFIRIDTACVLSRKAARR 240
QY 241 A 241
DB 241 A 241
RESULT 6
ID AAW26237 standard; Protein; 241 AA.
XX AAW26237;
XX
XX 16-MAR-1998 (first entry)
XX
XX Human preproNGF.
XX
XX Fusion protein; hydrophilic spacer; recombinant; expression system;
XX carboxypeptidase; preproNGF.
XX
XX Homo sapiens.
XX
XX W09728272-A1.
XX
XX 07-AUG-1997.
XX
XX 31-JAN-1997; 97WO-US01470.

XX 31-JAN-1996; 96US-0595043.
XX
XX (TECH-) TECHNOLOGENE INC.
XX
XX Sgarlato GD;
XX
XX WPI: 1997-402624/37.
XX N-PSDB; AAT80162.
XX
XX Recombinant protein expression system for fusion protein production
XX - useful for high quantity production of authentic recombinant
XX proteins
XX
XX Example 6; Page 140-141; 194pp; English.
XX
XX A novel recombinant vector has been developed which comprises a
XX nucleotide sequence encoding a fusion protein. The fusion protein
XX comprises three domains joined together in order, from N-terminus to
XX C-terminus, of a first domain comprising a protein of interest, a second
XX domain comprising a hydrophilic spacer and an affinity domain, each
XX domain comprising amino acid residues. The present sequence represents
XX human preproNGF, used in example 6 of the present invention. The
XX recombinant vector is used for the production of authentic recombinant
XX proteins of interest. The method of the invention is useful for the
XX expression of fusion proteins capable of isolation by affinity
XX chromatography in pro- or eukaryotic cells. This method allows
XX for the efficient cleavage and generation of authentic proteins of
XX interest that do not contain extraneous (i.e. non-naturally occurring)
XX amino acids.
SQ Sequence 241 AA;
Query Match 99.8%; Score 1265; DB 18; Length 241;
Best Local Similarity 99.6%; Pred. No. 1.6e-133;
Matches 240; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSMLFTLTITAFILGIAEPHSESNVPAAGHTIPQVHWTKLOHSIDTLARRARSAAPAIA 60
DB 1 MSMLFTLTITAFILGIAEPHSESNVPAAGHTIPQVHWTKLOHSIDTLARRARSAAPAIA 60
QY 61 ARVAGQTRNITVDPLPFKKRLRSPRYLFTSTOPPRAADTQDLDPEVGAAPFNRTRRSK 120
DB 61 ARVAGQTRNITVDPLPFKKRLRSPRYLFTSTOPPRAADTQDLDPEVGAAPFNRTRRSK 120
QY 121 RSSSHPIFRHGEPSVCDVSVMWGDXTATDIDKGEVMVLGEVINNSVFQYFEETKCR 180
DB 121 RSSSHPIFRHGEPSVCDVSVMWGDXTATDIDKGEVMVLGEVINNSVFQYFEETKCR 180
QY 181 DPNPVDGCGRIDSKKMNSTCTTHTFVKALTMDSKQAAWRFIRIDTACVLSRKAARR 240
DB 181 DPNPVDGCGRIDSKKMNSTCTTHTFVKALTMDSKQAAWRFIRIDTACVLSRKAARR 240
QY 241 A 241
DB 241 A 241
RESULT 7
ID AAW48886 standard; Protein; 241 AA.
XX AAW48886;
XX
XX 12-OCT-1998 (first entry)
XX
XX Human prepro-nerve growth factor beta chain.
XX
XX Neurotrophin; nerve growth factor; NGF; human; purification;
XX hydrophobic interaction chromatography.
XX
XX Homo sapiens.
XX
XX

FH	Key	Location/Qualifiers
PT	Protein	1..121 /label= Prepro_region
FT	Protein	122..241 /label= Mat_protein
FT	Modified-site	167 /note= "N-glycosylated"
FT	Region	179..189 /note= "conserved Cys-containing region involved in Cys knot motif"
FT	Region	229..231 /note= "conserved Cys-containing region involved in Cys knot motif"
PV		
PN	WO9821234-A2.	
XX		
PD	22-MAY-1998.	
PF		
PP	14-NOV-1997; 97MO-US21068.	
PR	29-MAY-1997; 97US-0047855.	
PR	15-NOV-1996; 96US-0030838.	
PA	(GETH) GENENTECH INC.	
PI	Beck JT, Burton LE, Schmelzer CH;	
DR	WPI, 1998-322333/28.	
XX		
PT	Isolation of neurotrophin(s) from, e.g. mis-folded or glycosylated variant(s) - using hydrophobic interaction chromatography,	
PT	optionally in combination with high performance cation exchange chromatography	
PS	Disclosure; Fig 4; 59pp; English.	
XX		
CC	This polypeptide comprises the human nerve growth factor (NGF)	
CC	beta chain precursor. Methods are provided for large-scale purification of neurotrophins, including mature NGF, suitable for clinical use. A claimed method comprises: (1) separating the neurotrophin from the other proteins using a hydrophobic interaction chromatography resin (HICR); and optionally (2) separating the neurotrophin from a chemical variant by high performance cation exchange chromatography (HPCEC). The processes can also be used for purification of e.g. mouse NGF (see AAM4887), brain-derived neurotrophic factor (see AAM4888), neurotrophin-4/5 (see AAM4889) and neurotrophin-3 (see AAM4889). The processes allow separation of neurotrophins from various undesirable misprocessed, misfolded, site, glycosylated or charge forms. They allow selective separation from their variants and other molecules, and from other polypeptides with high pi. The processes are applicable to starting materials from various sources, including fermentation broths or lysed bacterial or mammalian cells.	
SO	Sequence 241 AA:	
	Query Match 99.8%; Score 1265; DB 19; Length 241; Best Local Similarity 99.6%; Pred. No. 1.6e-133; Matches 240; Conservative 1; Mismatches 0; Indels 0; Gaps 0	
DQ	1 MSMLFYTLITFLIGIOAEPHEESNVPHGHITPOVMHTLQHSLDTALRRASAPAAIA 60	
DB	1 MSMLFYTLITFLIGIOAEPHEESNVPHGHITPOVMHTLQHSLDTALRRASAPAAIA 60	
DY	61 ARVAGQTENITVDPLPKKRLRSRVLPSTOPREADTOLDPEVGGAAPFSPTHSK 120	
DB	61 ARVAGQTENITVDPLPKKRLRSRVLPSTOPREADTOLDPEVGGAAPFNTHSK 120	
DY	121 RSSSHPIIHRGBSFVCSVSVMWGDKTTATIDIKGEVMVLGEVININNSVFXYFFETKCR 180	
DB	121 RSSSHPIIHRGBSFVCSVSVMWGDKTTATIDIKGEVMVLGEVININNSVFXYFFETKCR 180	
DY	181 DPNPDSGCRGIDSCHMNSYCCTHTTFVKALTMDGQAAMRIIRIIDTACVCYLAKRAVR 240	

Db		181 DPHPVDSGCRGIDSKMNSICTTTHTFKAALTMDGQAAWFIRIDTACVCVSRAAVRR	240
Oy	241 A 241		
Db	241 A 241		
ID	AAY07303 standard; Protein, 241 AA.		
XX	AAY07303		
AC	AAY07303;		
DT	06-JUL-1999 (first entry)		
DE	Human nerve growth factor beta protein.		
KX	Cerebrospinal; axon; growth; mammal; spinal cord injury; lesion; NGF2;		
KW	expression vector; neurotrophin; nerve growth factor 2; neurotrophin 3;		
KM	NT3; voluntary motor function.		
OS	Homo sapiens.		
PN	MOJ900148-A2.		
PD	07-JAN-1999.		
PZ	30-JUN-1998; 96WO-US13778.		
PR	30-JUN-1997; 97US-0051255.		
PA	(REGC) UNIV CALIFORNIA.		
PI	Gage FH, Grill R, Tuszynski MH;		
DR	MPL: 1999-095478/08.		
DX	N-PDBE; AAX34366.		
PT	Treating spinal cord injuries in a mammal - by inducing growth of		
PF	cerebrospinal projection axons using a recombinant vector for		
PP	expressing CST neurotrophin		
PS	Disclosure; Fig 6; 49pp; English.		
CC	The invention relates to a method of inducing cerebrospinal projection		
CC	(CST) axon growth in a mammal with a spinal cord injury that involves		
CC	a CST lesion by delivering a recombinant expression vector for CST		
CC	neurotrophin, such as this sequence - nerve growth factor beta. The		
CC	method is used to induce partial recovery of voluntary motor function		
CC	in a mammal after disruption of corticospinal projections in the spinal		
CC	cord.		
SQ	Sequence 241 AA;		
Oy	Query Match 99.8%; Score 1265; DB 20; Length 241;		
Db	Best Local Similarity 99.6%; Pred.No. 1.6e-133;		
Db	Matches 240; Conservative 1; Mismatches 0; Indels 0; Gaps 0;		
Oy	1 MSMLFYLLIAPFLIGIOAEPHSESNVAAGHTIPGVHWTKLOHSIDLTLRARRASAPAAAIA	60	
Db	1 MSMLFYLLIAPFLIGIOAEPHSESNVAAGHTIPGVHWTKLOHSIDLTLRARRASAPAAAIA	60	
Oy	ARVAGOTRINTVDPERLTKQRRLRSERVLPSTOPREAADODUDFEVGGAAPESRTSRK	120	
Db	61 ARVAGOTRINTVDPERLTKQRRLRSERVLPSTOPREAADODUDFEVGGAAPERTSRK	120	
Oy	RSSSHPIFHGEFSVCDVSVMWGDKTTATDINGKEVMVLGBVINNINSVFKOYFFETKCR	180	
Db	121 RSSSHPIFHGEFSVCDVSVMWGDKTTATDINGKEVMVLGBVINNINSVFKOYFFETKCR	180	
Oy	DHPHVDSGCGRIDSKMNSICTTTHTFKAALTMDGQAAWFIRIDTACVCVSRAAVRR	240	

DB 181 DENPVDSCGRGIDSKHMSYCTTHTFVKALTMGKQAMRPIRIDTACVCLSRKAVR 240

QY 241 A 241

DB 241 A 241

RESULT 9
AAB66929
ID AAB66929 standard; Protein; 241 AA.

AC AAB66929;
XX
XX
DT 17-APR-2001 (first entry)
XX
DE Human NGF.
XX
XX Human; neuroprotective; neuronal factor; NF; neurotrophin-3; NT-3;
KW neurodegenerative disease; Alzheimer's disease; Parkinson's disease;
KW Huntington's chorea; nerve damage; nerve growth factor; NGF.
OS Homo sapiens.
XX
XX US6174701-B1.
XX
XX 16-JAN-2001.
XX
XX 31-MAY-1995; 95US-0455741.
XX
XX 15-MAR-1990; 90US-0494024.
XX
XX 31-JAN-1995; 95US-0381030.
XX
XX 12-DEC-1989; 89US-0449811.
XX
XX (GETH) GENENTECH INC.
XX
XX Rosenthal A, Winelow JW;
XX
XX MPI; 2001-201803/20.
XX
XX New nucleic acid, encoding a neuronal factor (rat precursor
PT neurotrophin-3, NT-3), useful in the recombinant preparation of NT-3,
PT which is useful for enhancing the survival of nerve cells and treating
PT neurodegenerative diseases
XX
XX Disclosure; Fig 3; 18pp; English.
XX
XX The present invention relates to neuronal factor (NF; also known as
CC neurotrophin-3/NT-3; see AAF55829-AAF55830 and AAB66929-AA66928). NF
CC is useful in treating neurodegenerative diseases, e.g. Alzheimer's
CC disease, Parkinson's disease, Huntington's chorea, and other conditions
CC characterised by necrosis or loss of neurons. NF is also useful for
CC treating damaged nerves, e.g. nerves damaged by traumatic conditions such
CC as burns or wounds. The present sequence is human nerve growth factor
CC (NGF), which was used in a sequence homology alignment with human NF
CC protein.
XX
XX Sequence 241 AA;
SQ

Query Match 99.8%; Score 1265; DB 22; Length 241;
Best Local Similarity 99.6%; Pred. No. 1.6e-133;
Matches 240; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSMLFYTLITAFILGIOAEPSHSNVPAGHTIPOVHWTXQHSIDTLARRARSPAAIA 60
DB 1 MSMLFYTLITAFILGIOAEPSHSNVPAGHTIPOVHWTXQHSIDTLARRARSPAAIA 60

QY 61 ARVAGGTNTITVDPRLFKKRLRSRVLFTSTOPREAADTODLDFEVGGAAPFRTTRSK 120
DB 61 ARVAGGTNTITVDPRLFKKRLRSRVLFTSTOPREAADTODLDFEVGGAAPFRTTRSK 120

QY 121 RSSHPITFRGGEFVSVDVSVWVGDKTATDICKGEVWVLGEVWINSVFQYFFETKCR 180
DB 121 RSSHPITFRGGEFVSVDVSVWVGDKTATDICKGEVWVLGEVWINSVFQYFFETKCR 180

QY 181 DENPVDSCGRGIDSKHMSYCTTHTFVKALTMGKQAMRPIRIDTACVCLSRKAVR 240

DB 181 DENPVDSCGRGIDSKHMSYCTTHTFVKALTMGKQAMRPIRIDTACVCLSRKAVR 240

QY 241 A 241

DB 241 A 241

RESULT 10
AAB18904
ID AAB18904 standard; Protein; 241 AA.

AC AAB18904;
XX
XX
DT 21-MAY-2002 (first entry)
XX
DE Human beta nerve growth factor (NGF) protein.
XX
XX Human; nerve growth factor; NGF; neurotrophin; cholinergic neuron;
KW gene therapy; neuroprotective; Alzheimer's disease; Parkinson's disease;
KW neurodegenerative condition; ALS; amyotrophic lateral sclerosis.
XX
XX Homo sapiens.
XX
XX WO200207774-A2.
XX
XX 31-JAN-2002.
XX
XX 17-MAY-2001; 2001WO-US16122.
XX
XX 19-JUL-2000; 2000US-0620174.
XX
XX (REGC) UNIV CALIFORNIA.
XX
XX Tuszynski MH;
XX
XX MPI; 2002-195846/25.
XX
XX N-PSDB; AAD30144.
XX
XX Delivering therapeutic neurotrophin to targeted defective, diseased or
PT damaged cholinergic neurons, useful for treating neurodegenerative
PT disease, comprises administering a neurotrophin encoding transgene into
PT the brain
XX
XX Example 1; Fig 2; 38pp; English.
XX
XX The invention relates to a method for delivering therapeutic neurotrophin
CC to targeted defective, diseased or damaged cholinergic neurons in
CC the mammalian brain. The method comprises delivering a neurotrophin
CC composition comprising a neurotrophin encoding transgene into one or more
CC delivery sites within a region of the brain containing targeted neurons.
CC The method is useful for treating neurodegenerative conditions such as
CC Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis
CC (ALS) in primates by stimulating the growth of neurons thus recovering
CC neurological function. The present sequence is human nerve growth factor
CC (NGF-2) protein which is a neurotrophin.
XX
XX Sequence 241 AA;
SQ

Query Match 99.8%; Score 1265; DB 23; Length 241;
Best Local Similarity 99.6%; Pred. No. 1.6e-133;
Matches 240; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSMLFYTLITAFILGIOAEPSHSNVPAGHTIPOVHWTXQHSIDTLARRARSPAAIA 60
DB 1 MSMLFYTLITAFILGIOAEPSHSNVPAGHTIPOVHWTXQHSIDTLARRARSPAAIA 60

QY 61 ARVAGGTNTITVDPRLFKKRLRSRVLFTSTOPREAADTODLDFEVGGAAPFRTTRSK 120
DB 61 ARVAGGTNTITVDPRLFKKRLRSRVLFTSTOPREAADTODLDFEVGGAAPFRTTRSK 120

QY 121 RSSSHPIFRHGEFVCDVSVMVGDKTTATDICKENMVLGEVINNSVFKQYFFETKCR 180
 DB 121 RSSSHPIFRHGEFVCDVSVMVGDKTTATDICKENMVLGEVINNSVFKQYFFETKCR 180
 QY 181 DPNPVDSCGCGIDSKHNSYCTTTHTFVKALTMGKQAMRFIRIDTACVCLSRKAVRR 240
 DB 181 DPNPVDSCGCGIDSKHNSYCTTTHTFVKALTMGKQAMRFIRIDTACVCLSRKAVRR 240
 QY 241 A 241
 DB 241 A 241
 RESULT 11
 ABB04994
 ID ABB04994 standard; Protein; 241 AA.
 AC ABB04994;
 DT 19-MAR-2002 (first entry)
 DE Human beta nerve growth factor protein.
 KM Human; nerve growth factor 2; beta nerve growth factor; NGF-2; NT-3;
 KM neurotrophin-3; nervous system growth factor; neuronal atrophy;
 KM aging; brain; axonal growth; neuron; neurotrophic; neuroprotective;
 KM anti-aging; cholinergic neuron growth stimulator; gene therapy.
 OS Homo sapiens.
 XX US2001043920-A1.
 PN 22-NOV-2001.
 PD 05-DEC-2000; 2000US-0730790.
 PF 15-APR-1998; 98US-0060543.
 PR (TUSZ/) TUSZYNSKI M H.
 PA (BLES/) BLESCH A.
 XX Tuszynski MH, Blesch A;
 PI WPI, 2002-105567/14.
 DR N-PSDB; ABA92503.
 XX Ameliorating neuronal atrophy and loss of accompanying normal aging
 PT comprises delivering a transgene encoding a growth factor to a
 PT mammalian brain to stimulate axon growth in cholinergic neurons
 PS Disclosure; Fig 6 1-2; 18pp; English.
 XX The present invention describes a method for ameliorating neuronal
 CC atrophy and loss of accompanying normal aging in the mammalian brain.
 CC The method comprises delivering a growth factor (GF)-encoding transgene
 CC to preslected delivery sites in the brain, so that the encoded GF is
 CC expressed in the brain and stimulates axonal growth in targeted
 CC GF-receptive neurons. The growth factor has neurotrophic, neuroprotective
 CC and anti-aging activities, and can be used as a cholinergic neuron
 CC growth stimulator and in gene therapy. The method is used to
 CC ameliorating neuronal atrophy and loss of accompanying normal aging, in
 CC the human brain. The present sequence represents human beta nerve growth
 CC factor, which is given in the exemplification of the present invention.
 XX
 SQ Sequence 241 AA;
 Query Match 99.8%; Score 1265; DB 23; Length 241;
 Best Local Similarity 99.6%; Pred. No. 1.6e-133;
 Matches 240; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSMLFTTLTATLALIGIOAPHSSESNVPAGHTTIPQVHTKLOHSLDTALRRARSAPAAIA 60
 DB 1 MSMLFTTLTALFLIGIOAPHSSESNVPAGHTTIPQVHTKLOHSLDTALRRARSAPAAIA 60

QY 1 MSMLFTTLTATLALIGIOAPHSSESNVPAGHTTIPQVHTKLOHSLDTALRRARSAPAAIA 60
 DB 1 MSMLFTTLTALFLIGIOAPHSSESNVPAGHTTIPQVHTKLOHSLDTALRRARSAPAAIA 60

QY 61 ARVAGQTNITVDBRLFEKRLRSPRVLFSTOPPRAADTODDLFEVGAAPSRTRRSK 120
 DB 61 ARVAGQTNITVDBRLFEKRLRSPRVLFSTOPPRAADTODDLFEVGAAPSRTRRSK 120
 QY 121 RSSSHPIFRHGEFVCDVSVMVGDKTTATDICKENMVLGEVINNSVFKQYFFETKCR 180
 DB 121 RSSSHPIFRHGEFVCDVSVMVGDKTTATDICKENMVLGEVINNSVFKQYFFETKCR 180
 QY 241 A 241
 DB 241 A 241
 RESULT 12
 AAP40038
 ID AAP40038 standard; Protein; 245 AA.
 AC AAP40038;
 DT 25-JAN-1992 (first entry)
 DE Sequence encoded by portion of human beta-nerve growth factor
 DE (NGF) chromosomal gene which includes an exon.
 OS Nerve damage; therapy.
 XX Homo sapiens.
 PN EP121338-A.
 PD 10-OCT-1984.
 PF 02-MAR-1984; 84EP-0301377.
 PR 03-MAR-1983; 83US-0471962.
 PA (GETH) GENENTECH INC.
 XX Gray AM, Ullrich A;
 PI WPI, 1984-251909/41.
 DR N-PSDB; AAN40033.
 XX Human beta-nerve growth factor free from other proteins - obcd.
 PT by recombinant DNA techniques for treating nerve damage
 PS Example; Fig 5; 42pp; English.
 XX The inventors claim human beta-nerve growth factor (NGF) free from
 CC other proteins of human origin. Also claimed are the DNA sequence
 CC encoding human beta-NGF operably linked with a DNA sequence capable
 CC of effecting its expression in a recombinant host cell; a replicable
 CC expression vector contg. the DNA; and host cells transformed with
 CC the vector. The plasmid claimed is plasmid ph-beta-NGF trp 1. Using
 CC the plasmid, larger amounts of pure beta-NGF are obtainable than by
 CC extrn. of natural materials, see e.g. EP--2139.
 XX
 SQ Sequence 245 AA;
 Query Match 99.8%; Score 1265; DB 5; Length 245;
 Best Local Similarity 99.6%; Pred. No. 1.7e-133;
 Matches 240; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSMLFTTLTATLALIGIOAPHSSESNVPAGHTTIPQVHTKLOHSLDTALRRARSAPAAIA 60
 DB 5 MSMLFTTLTALFLIGIOAPHSSESNVPAGHTTIPQVHTKLOHSLDTALRRARSAPAAIA 64
 QY 61 ARVAGQTNITVDBRLFEKRLRSPRVLFSTOPPRAADTODDLFEVGAAPSRTRRSK 120

QY 1 MSMLFTTLTATLALIGIOAPHSSESNVPAGHTTIPQVHTKLOHSLDTALRRARSAPAAIA 60
 DB 5 MSMLFTTLTALFLIGIOAPHSSESNVPAGHTTIPQVHTKLOHSLDTALRRARSAPAAIA 64
 QY 61 ARVAGQTNITVDBRLFEKRLRSPRVLFSTOPPRAADTODDLFEVGAAPSRTRRSK 120

Db 65 ARVAGQTRNITVDPRLFKKRLRSPRVLFSTQPPREAADTODLDEVEGGAAPFNTRHSK 124
Qy 121 RSSSHPIFRHGFSPVCDVSVMVGDXTATIDIKGEVWVLGEVINNSVFKQYFFETKCR 180
Db 125 RSSSHPIFRHGFSPVCDVSVMVGDXTATIDIKGEVWVLGEVINNSVFKQYFFETKCR 184
Qy 181 DPNPVDSCGRGIDSKMNSYCTTHTTFVKALTMQKQAMRFRIDTACVCLSRKAVR 240
Db 185 DPNPVDSCGRGIDSKMNSYCTTHTTFVKALTMQKQAMRFRIDTACVCLSRKAVR 244
Qy 241 A 241
Db 245 A 245

RESULT 13

AAR45241
ID AAR45241 standard; Protein; 307 AA.

AC AAR45241;
DT 20-JUN-1994 (first entry)
DE Human pre-pro nerve growth factor.
KW Mature; beta-nerve growth factor; pre-pro portion;
expression; NGF; hNGF; treatment; Alzheimer's Disease.
OS Homo sapiens.
PH Key Location/Qualifiers
FT Peptide 1..187.
FT Peptide /note= "signal peptide"
FT Peptide 188..307
FT Peptide /note= "mature peptide"
PN US5272063-A.
PD 21-DEC-1993.
PF 20-JUN-1989; 89US-0383118.
PR 22-NOV-1988; 88US-0274878.
PR 20-JUL-1989; 89US-0383118.
PA (SYNT) SYNTAX USA INC.
PI Baecker PA, Barnett JW, BursztyN-Pettegrew H, Chan HW, Nguyen BT,
Ward C;
PI WPI; 1993-413401/51.
DR N-PSDB; AAO54283.
XX Prodn. of active mature human beta-nerve growth factor in insect
XX cells - using baculovirus expression system, and potential use of
XX recombinant hNGF in treatment of Alzheimer's disease
XX Disclosure; Fig 1; 23pp; English.
XX The sequence is that of human pre-pro nerve growth factor
XX which was used in a method of producing biologically active
XX mature human beta-nerve growth factor in insect cells.
SQ Sequence 307 AA;

Query Match 99.5%; Score 1262; DB 1; Length 307;
Best Local Similarity 99.2%; Pred. No. 5e-133;
Matches 239; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSMLFYTLITAFILGIAQEPHSESNVPAGHTIIPVHWTKLOHSLDTLRARSAAPAAIA 60
Db 67 MSMLFYTLITAFILGIAQEPHSESNVPAGHTIIPVHWTKLOHSLDTLRARSAAPAAIA 126

Qy 61 ARVAGQTRNITVDPRLFKKRLRSPRVLFSTQPPREAADTODLDEVEGGAAPFNTRHSK 120
Db 127 ARVAGQTRNITVDPRLFKKRLRSPRVLFSTQPPREAADTODLDEVEGGAAPFNTRHSK 186
Qy 121 RSSSHPIFRHGFSPVCDVSVMVGDXTATIDIKGEVWVLGEVINNSVFKQYFFETKCR 180
Db 187 RSSSHPIFRHGFSPVCDVSVMVGDXTATIDIKGEVWVLGEVINNSVFKQYFFETKCR 246
Qy 181 DPNPVDSCGRGIDSKMNSYCTTHTTFVKALTMQKQAMRFRIDTACVCLSRKAVR 240
Db 247 DPNPVDSCGRGIDSKMNSYCTTHTTFVKALTMQKQAMRFRIDTACVCLSRKAVR 306
Qy 241 A 241
Db 307 A 307

RESULT 14

AAB67865
ID AAB67865 standard; Protein; 241 AA.

AC AAB67865;
DT 29-JUN-2001 (first entry)

DE Amino acid sequence of a human polypeptide designated PTMA-8.
KW PTMA; immune deficiency; infection; autoimmune disorder; wound closure;
connective tissue disease; multiple sclerosis; rheumatoid arthritis;
systemic lupus erythematosus; autoimmune pulmonary inflammation; ulcer;
Guillian-Barre syndrome; autoimmune thyroiditis; myasthenia gravis;
insulin dependent diabetes mellitus; graft-versus-host disease;
autoimmune inflammatory eye disease; gut protection; gut regeneration;
fibrosis; reperfusion injury; systemic cytokine damage.
OS Homo sapiens.
PN WO200123572-A2.
PD 05-APR-2001.
PF 29-SEP-2000; 2000WO-US41035.
PR 30-SEP-1999; 99US-0156745.
PR 06-OCT-1999; 99US-0158942.
PR 13-OCT-1999; 99US-0159248.
PR 06-DEC-1999; 99US-0169344.
PR 29-JUN-2000; 2000US-0215048.

PA (CURA-) CURAGEN CORP.
PI Prayaga SK, Vernet C, Shimkets RA, Burgess C, Spytek KA;
WPI; 2001-273512/28.
DR N-PSDB; AAF60462.
XX Novel polypeptides termed PTMAX, and nucleic acids encoding PTMAX,
XX useful for detecting and treating diseases caused immune deficiencies -
XX Claim 1; Page 20-22; 128pp; English.
XX The present sequence represents a PTMA-8 (not defined) polypeptide. The
XX sequence is derived from clone AL049825. The polypeptide is 2658.5
XX daltons. PTMA polynucleotides and polypeptides are used in the
XX manufacture of a medicament for treating a syndrome associated with a
XX human disease, the disease selected from a pathology associated with a
XX PTMA. They may be useful in the treatment of various immune deficiencies
XX and disorders. These immune deficiencies may be genetic or caused by
XX viral as well as bacterial or fungal infections or may result from
XX autoimmune disorders. Autoimmune disorders which may be treated using
XX PTMA include, for example, connective tissue disease, multiple sclerosis,
XX systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary

CC inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin
 CC dependent diabetes mellitus, myasthenia gravis, graft-versus-host disease
 CC and autoimmune inflammatory eye disease. Additionally, PTMA may also be
 CC useful to promote better or faster closure of non-healing wounds,
 CC including pressure ulcers, ulcers associated with vascular insufficiency,
 CC surgical and traumatic wounds. Furthermore, PTMA may also be useful for
 CC gut protection or regeneration and treatment of lung or liver fibrosis,
 CC reperfusion injury in various tissue, and conditions resulting from
 CC systemic cytokine damage.

XX Sequence 241 AA;

Query Match 99.4%; Score 1261; DB 22; Length 241;

Best Local Similarity 99.2%; Pred. No. 4, 6e-133;

Matches 239; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSMLPYTLITAFLLIGIOAEPPHSESNVPAGHTIPQVHWTKLOHSIDTLARRASAPAAIA 60

DB 1 MSMLPYTLITAFLLIGIOAEPPHSESNVPAGHTIPQVHWTKLOHSIDTLARRASAPAAIA 60

QY 61 ARVAGQNTITVDRLFKKRLRSRVLFSSTOPPREAADTODLDFEVGAAPFSRTHRSK 120

DB 61 ARVAGQNTITVDRLFKKRLRSRVLFSSTOPPREAADTODLDFEVGAAPFSRTHRSK 120

QY 121 RSSSHPIFRHGEFVCDVSVMVGDKTTATDICKKENVLGEVINNSVFKQYFFETKCR 180

DB 121 RSSSHPIFRHGEFVCDVSVMVGDKTTATDICKKENVLGEVINNSVFKQYFFETKCR 180

QY 181 DPNVDGCGRIGDSKHNNSYCTTHTFFVKALTMDSKQAAFRIRIDTACVLSKAVRR 240

DB 181 DPNVDGCGRIGDSKHNNSYCTTHTFFVKALTMDSKQAAFRIRIDTACVLSKAVRR 240

QY 241 A 241

DB 241 A 241

RESULT 15

AAR37799 standard; Protein; 307 AA.

XX AAR37799;

DT 23-SEP-1993 (first entry)

XX Human NGF.

XX Chimeric; human; prepro; NGF; brain-derived neurotrophic factor;

KM BDNF; chimera; fusion; mouse; nerve growth factor; peripheral;

XX central; precursor; nervous system.

OS Homo sapiens.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Region 1..187

FT Protein /note="Prepro region"

FT /note="188..307"

XX /note="Mature NGF"

XX MO9310150-A.

XX 27-MAY-1993.

XX 13-NOV-1992; 92MO-US09792.

XX 14-NOV-1991; 91US-0792492.

XX (AMGS-) AMGEN.

XX (REG-) REGENERON PHARM INC.

XX Gies D, Hu SS, Ip N, Squinto SP, Yancopoulos GD;

XX WPI; 1993-182492/22.

DR N-PSDB; AAQ42571.

XX Eukaryotic expression of neurotrophins - using prepro region of a

PT different neurotrophin for more efficient post-translational

XX processing

PS Disclosure; Fig 4; 80pp; English.

XX This sequence represents human nerve growth factor (NGF). The protein
 CC encoded by this sequence promotes the development of the peripheral
 CC nervous system and also influences the development and maintenance of
 CC specific populations of neurons in the central nervous system. Two
 CC major transcripts from the NGF gene result in a "long" and "short" NGF
 CC prepropeptide. The "short" precursor contains a conventional signal
 CC sequence at the N-terminus which flanks the pro-region. The "long"
 CC precursor contains an additional "pro-region" at its N-terminal. No
 CC functional distinction has been elucidated between the "long" and
 CC "short" forms. Characteristics of NGF, such as isoelectric point and
 CC primary structure, are very similar to brain derived neurotrophic
 CC factor (BDNF). The NGF coding sequence may be used in the
 CC construction of a chimeric nucleic acid molecule to encode a prepro-
 CC NGF/BDNF chimera (see also AAQ42568-69).

XX Sequence 307 AA;

Query Match 99.4%; Score 1261; DB 14; Length 307;

Best Local Similarity 99.2%; Pred. No. 6, 5e-133;

Matches 239; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSMLPYTLITAFLLIGIOAEPPHSESNVPAGHTIPQVHWTKLOHSIDTLARRASAPAAIA 60

DB 67 MSMLPYTLITAFLLIGIOAEPPHSESNVPAGHTIPQVHWTKLOHSIDTLARRASAPAAIA 126

QY 61 ARVAGQNTITVDRLFKKRLRSRVLFSSTOPPREAADTODLDFEVGAAPFSRTHRSK 120

DB 127 ARVAGQNTITVDRLFKKRLRSRVLFSSTOPPREAADTODLDFEVGAAPFSRTHRSK 186

QY 121 RSSSHPIFRHGEFVCDVSVMVGDKTTATDICKKENVLGEVINNSVFKQYFFETKCR 180

DB 187 RSSSHPIFRHGEFVCDVSVMVGDKTTATDICKKENVLGEVINNSVFKQYFFETKCR 246

QY 181 DPNVDGCGRIGDSKHNNSYCTTHTFFVKALTMDSKQAAFRIRIDTACVLSKAVRR 240

DB 247 DPNVDGCGRIGDSKHNNSYCTTHTFFVKALTMDSKQAAFRIRIDTACVLSKAVRR 306

QY 241 A 241

DB 307 A 307

Search completed: June 6, 2003, 10:49:31

Job time : 33.5 secs